

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:07:08 ; Search time 113.31 Seconds

(without alignments)
9.081 Million cell updates/sec

Title: US-09-165-546A-10

Perfect score: 92

Sequence: 1 PLPVPGVLLIKEFTVSGNI 18

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters:

165078

Post-processing: Minimum Match 0%

Minimum DB seq length: 0

Maximum DB seq length: 25

Listing first 45 summaries

Database : A_Geneseq_0401;*

1: /SDS6/gcgdata/geneseq/geneseqp/AA1980.DAT;*
 2: /SDS6/gcgdata/geneseq/geneseqp/AA1981.DAT;*
 3: /SDS6/gcgdata/geneseq/geneseqp/AA1982.DAT;*
 4: /SDS6/gcgdata/geneseq/geneseqp/AA1983.DAT;*
 5: /SDS6/gcgdata/geneseq/geneseqp/AA1984.DAT;*
 6: /SDS6/gcgdata/geneseq/geneseqp/AA1985.DAT;*
 7: /SDS6/gcgdata/geneseq/geneseqp/AA1986.DAT;*
 8: /SDS6/gcgdata/geneseq/geneseqp/AA1987.DAT;*
 9: /SDS6/gcgdata/geneseq/geneseqp/AA1988.DAT;*
 10: /SDS6/gcgdata/geneseq/geneseqp/AA1989.DAT;*
 11: /SDS6/gcgdata/geneseq/geneseqp/AA1990.DAT;*
 12: /SDS6/gcgdata/geneseq/geneseqp/AA1991.DAT;*
 13: /SDS6/gcgdata/geneseq/geneseqp/AA1992.DAT;*
 14: /SDS6/gcgdata/geneseq/geneseqp/AA1993.DAT;*
 15: /SDS6/gcgdata/geneseq/geneseqp/AA1994.DAT;*
 16: /SDS6/gcgdata/geneseq/geneseqp/AA1995.DAT;*
 17: /SDS6/gcgdata/geneseq/geneseqp/AA1996.DAT;*
 18: /SDS6/gcgdata/geneseq/geneseqp/AA1997.DAT;*
 19: /SDS6/gcgdata/geneseq/geneseqp/AA1998.DAT;*
 20: /SDS6/gcgdata/geneseq/geneseqp/AA1999.DAT;*
 21: /SDS6/gcgdata/geneseq/geneseqp/AA2000.DAT;*
 22: /SDS6/gcgdata/geneseq/geneseqp/AA2001.DAT;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	81.5	88.6	19 21	Y52437 Human tumour antigen
2	52	56.5	10 20	Y05998 Human cancer antigen
3	45	48.9	9 20	Y06026 Human cancer antigen
4	43	46.7	9 20	Y06027 Human cancer antigen
5	41.5	45.1	17 21	Y52436 Human tumour antigen
6	37	40.2	9 16	R82133 Melanoma specific antigenic site of NY-ESO-1 derived peptide
7	37	40.2	23 20	W97452 Human cancer antigen
8	35	38.0	9 21	Y79153 Melanoma specific antigenic site of NY-ESO-1 derived peptide
9	35	38.0	10 20	Y06001 Human cancer antigen
10	33	35.9	9 16	R82132 Melanoma specific antigenic site of NY-ESO-1 derived peptide
11	33	35.9	10 16	R82174 Melanoma specific antigenic site of NY-ESO-1 derived peptide

Synthetic.

Homo sapiens.

W0953938-A1.

XX

ALIGNMENTS

RESULT 1	Y52437	ID Y52437 standard; Protein; 19 AA.
XX	XX	Human tumour antigen NY-ESO-1 peptide #10.
AC	AC	
XX	XX	
XX	XX	15-FEB-2000 (first entry)

XX	XX	DE Human tumour antigen NY-ESO-1 peptide #10.
XX	XX	KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
XX	XX	KW T-cell; helper; stimulation; proliferation; treatment;
XX	XX	KW prostate cancer; prevention; melanoma; breast cancer; ovarian cancer; bladder cancer; lung cancer; lymphoma.
XX	XX	KW Synthetic.

Homo sapiens.

OS

SH3-binding peptid

PPPP motif contai

Peptide resembling

Reagent of GTP-bin

Human P160 interna

Human peptide HKV1

Antigenic site of

Mammalian ion chan

Fragment of human

Human CERB2 oncoge

Human CERB2 oncoge

Immunogenic peptid

Immunogenic peptide

Human CERB2 oncoge

Immunogenic peptid

Human CERB2 oncoge

Human CERB2 oncoge

Human secreted pro

Potato THIN protein

SH3 domain in bin

Src SH3 domain bind

SH3 synthetic bind

Murine stromalin-1

SH3 domain peptide

FDF-5 mutant pepti

FDF-5 mutant pepti

Human cytomegalovi

Human cytomegalovi

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX Claim 4; Page 22; 49pp; English.
XX Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (Y2430) which can bind to MHC major
histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
isolated from an oesophagus squamous cell cancer cDNA library. Tissue
localisation studies revealed it to be expressed at high levels
in normal ovary and testis but not in normal colon, kidney, liver,
brain, oesophagus and skin. It was expressed in certain tumours and
tumour cell lines with some degree of frequency - these included
melanoma specimens and cell lines, and breast and bladder cancer
specimens, with expression in other tumour types being sporadic.
These NY-ESO-1-derived peptides may be used in methods and
compositions for the treatment, diagnosis and prevention of
cancers (such as melanoma, breast cancer, prostate cancer, lung
cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
or lymphoma) and to stimulate the proliferation of T cells.
XX Sequence 19 AA;

Query Match 88.6%; Score 81.5; DB 21; Length 19;
Best Local Similarity 94.7%; Pred. No 1.1e-07; Indels 1; Gaps 1;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query 1 PLPVPGVLL-KERTVSGNI 18
ID Y05998 standard; Peptide; 10 AA.
Db 1 plpvpgvllkkkertvsgni 19

RESULT 2
Y05998
ID Y05998 standard; Peptide; 10 AA.

AC Y05998;
XX 16-AUG-1999 (first entry)
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
Homo sapiens.
OS Homo sapiens.
PN W0918206-A2.
PD 15-APR-1999.
XX 21-SEP-1998; 98WO-US19609.
XX 08-OCT-1997; 97US-0061428.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rosenberg SA, Wang RF;
XX DR WPI; 1999-277270/23.
XX Cancer antigen NY ESO1/CAG-3
Example 10; Page 42; 88pp; English.
XX PS

CC This peptide was identified as an HLA peptide motif following a
screen for epitopes from the coding region of human ESO-1/CAG-3
ORF1 (see X58599). 30 Epitopes (see Y05888-Y06017) were identified.
CC The present peptide (ranked 11) corresponds to amino acid residues
115-124 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent
tumour antigen capable of eliciting an antigen specific immune
response by T cells. Cancer peptides (see Y05967-87) derived from
CAG-3, portions of CAG-3 and their variants, are useful as cancer
vaccines. A claimed method of preventing or inhibiting cancer
administration of a cancer peptide, with or without an HLA
molecule. The cancer peptides form part of, or are derived
from, cancers such as primary or metastatic melanoma, thymoma,
lymphoma, carcinoma, lung cancer, liver cancer, leukaemia, uterine
cancer, cervical cancer, bladder cancer, kidney cancer and
adenocarcinomas such as breast, prostate, ovarian, pancreatic and
thyroid cancers.
XX SQ Sequence 10 AA;
XX Query Match 56.5%; Score 52; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0e+0; Mismatches 0; Indels 0; Gaps 0;

CC This peptide was identified as an HLA peptide motif following a
screen for epitopes from the coding region of human ESO-1/CAG-3
ORF1 (see X58599). 30 Epitopes (see Y06018-47) were identified.
CC The present peptide (ranked 9) corresponds to amino acid residues
116-124 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent
tumour antigen capable of eliciting an antigen specific immune

CC	lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.
XX	Sequence 9 AA;
	Query Match 5
	Y52436 Best Local Similarity 46.7%; Score 43; DB 20; Length 9; Matches 9; Conservative 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gap 0;
Oy	6 GVLKEFTV 14 1 gvlkeftv 9
Db	AC Y52436; XX DT 15-FEB-2000 (first entry) XX Human tumour antigen NY-ESO-1 peptide #9. XX Cancer; tumour antigen; MHC; major histocompatibility complex; Class I-cell; helper; stimulation; proliferation; treatment; KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer; KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; KW lymphoma. XX Synthetic, OS Homo sapiens. XX W09953938-A1. XX PD 28-OCT-1999. XX PF 24-MAR-1999; 99WO-US06875. XX PR 17-APR-1998; 98US-0062422. XX PR 02-OCT-1998; 98US-0165546. PA (LUDWIG INST CANCER RES. XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ; PI Gure A, Ritter G; XX DR; 2000-038483/03. XX Novel peptides which bind to MHC class I and MHC class III molecule useful for therapeutic and diagnostic purposes - XX Claim 4; Page 22; 49pp; English. PS Peptides # 8-#13 (Y52435-Y52440) are peptides derived from the human tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC(class I) major histocompatibility Class II HLA-DP3 molecules, thereby stimulating proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and melanoma cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.

Melanoma-specific immunogen comprises epitope(s) homologous with pMEL-17 - are highly potent stimulators of HLA-A2+CTL's useful in adoptive immuno-therapy

PT Example 8; Page 51; 148pp; English.

PT A melanoma-specific immunogen homologous with pMEL-17 comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the group R82098-R82194 capable of eliciting a CTL response. The epitopes R82098-R82108 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma. Peptides which are homologous with pMEL-17 are highly potent stimulators of HLA-A2+ CTLs in several cell lines and can be used in immunotherapy or incorporated into immunogenic conjugates as vaccines.

SQ Sequence 9 AA;

Query	Match	Score 33;	DB 16;	Length 10;
Best Local Matches	Local Similarity 5;	Pred. No. 16;	Score 33;	DB 16;
Matches	Conservative 2;	Mismatches 0;	Score 33;	DB 16;
Qy	2 LPVPGVL 8	Indels 0;	Score 33;	DB 16;
CC	: :	Gaps 0;	Score 33;	DB 16;
CC	Db	4 mpvpgl 10	Score 33;	DB 16;

RESULT 12
ID W05451 standard; Peptide: 15 AA.
XX XX
AC W05451;
XX XX
DT 24-FEB-1998 (first entry)
XX DE SH3-binding Peptide bSH3002.
XX KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process; binding peptide.
XX OS Synthetic.
XX XX
AC W09631625-A1.
XX XX
AC W09631625-A1.
XX PD 10-OCT-1996.
XX PF 04-APR-1996; 96WO-US04454.
XX PR 03-APR-1996; 96US-0630915.
DE 07-APR-1995;
XX PA (CYTO-) CYTOGEN CORP.
PA (UYN-C-) UNIV NORTH CAROLINA.
XX PI Fowlkes DM, Hoffman N, Kay BK, Mcconnell SJ, Sparks AB;
XX XX
AC W09522561-A2.
XX DR WPI: 1996-465045/46.
XX PT Identifying polypeptide(s) having specific functional domain (esp. SH3 domain) - comprises detecting selective binding to recognition unit, regardless of sequence homology
XX XX
AC W05445-W05492 represent Src-homology region 3 (SH2) domain binding peptides. These sequences were used as parts of multivalent recognition unit complexes used in the method of the invention. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). It comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins containing SH3 domains. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins homologous among known SH3 proteins. Multivalent RU complexes are CC particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in sequence to, the original target functional domain. The new method enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. pharmacological activities) can be assessed using the method of the invention.

PS Example 8; Page 52; 148pp; English.

PT A melanoma-specific immunogen homologous with pMEL-17 comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the group R82098-R82194 capable of eliciting a CTL response. The epitopes R82098-R82108 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma. Peptides which are homologous with pMEL-17 are highly potent stimulators of HLA-A2+ CTLs in several cell lines and can be used in immunotherapy or incorporated into immunogenic conjugates as vaccines.

SQ Sequence 10 AA;

Db 9 plpdpgv 15
 RESULT 15
 R04057 ID R04057 standard; peptide; 20 AA.
 XX AC R04057;
 XX DT 17-MAR-1993 (first entry)
 XX DE Reagent of GTP-binding protein (10).
 XX KW G-protein; signal transducing protein; cell proliferation;
 XX cancer; dementia; receptor; transmission.
 OS Synthetic.
 XX JP02069665-A.
 XX PD 08-MAR-1990.
 XX PP 06-SEP-1988; 88JP-0221446.
 XX PR 06-SEP-1988; 88JP-0221446.
 XX PA (NISHI/) NISHIMOTO I.
 XX DR 1990-11-19771/16.
 XX PT Reagent of GTP-binding protein - consists of polypeptide of less
 PT than 33 aminoacid residues where 4 are basic aminoacid residues,
 PT etc.
 XX Disclosure: Fig 1; 4pp; Japanese.
 XX A reagent for activating GTP-binding Protein (G-protein) consists of
 CC a polypeptide of less than 33 amino acids, of which more than 4 are
 CC basic, and more than 20₈ are hydrophobic. The reagent is useful for
 CC the purification, identification, functional examination, etc. of
 CC G-protein, a signal transducing protein. It will be possible to
 CC study the mechanism of cell proliferation, anticancer action,
 CC prevention of dementia, by activating/inhibiting the G-protein,
 CC using the reagent.
 CC The peptides given in R04048-59, R05848, R09313 and indicated in
 CC the Features table bind selectively, activating the G-protein. The
 CC peptides have the same config. as the part of the receptor which binds
 CC to G-protein and is effective for the transmission of signal information
 CC into the cell. The reagent can be used in the form of powder or soln.
 CC Affinity purification can be simply carried out by using ion-exchange
 CC resin beads such as Sepharose. For example, the reagent is stuck onto
 CC the beads and homogenate is passed through a column packed with the
 CC beads to obtain a given G-binding protein.
 XX Sequence 20 AA;

Query Match 34.88; Score 32; DB 11; Length 20;
 Best Local Similarity 53.8%; Pred. No. 54;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 LPVPGVILKEETV 14
 | ||:|||:
 Db 7 laarnvlvkdfiv 19

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OM protein - protein search, using sw mode.

Run on: May 8, 2001, 15:08:20 ; search time 68.24 Seconds

(without alignments)
18.127 Million cell updates/sec

Title: US-09-165-546A-10

Perfect score: 92
Sequence: 1 PLVPVGVLKEFTVSGNI 18Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters:

4929

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_671:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
5: pir5:
6: pir6:
7: pir7:
8: pir8:
9: pir9:
10: pir10:
11: pir11:
12: pir12:
13: pir13:
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16: pir16:
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18: pir18:
19: pir19:
20: pir20:
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23: pir23:
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28: pir28:
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31: pir31:
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34: pir34:
35: pir35:
36: pir36:
37: pir37:
38: pir38:
39: pir39:
40: pir40:
41: pir41:
42: pir42:
43: pir43:
44: pir44:
45: pir45:

RESULT 1

S13974

chlorophyll a/b-binding protein type I - garden pea (fragment)

C;Species: Pisum sativum (Garden pea)

C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C;Accession: S13974

R;Jahns, P.; Junge, W.

Eur. J. Biochem. 1993, 731-736, 1990

A;Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of th

A;Reference number: S13973; MUID:91065379

A;Accession: S13974

A;Molecule type: protein

A;Residues: 1-18 <JAH>

C;Genetics:

A;Genome: nuclear

C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem I; thylak

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	39.1	18	S13974	chlorophyll a/b-binding protein type I - garden pea (fragment)
2	30	32.6	20	S29817	cyclochrome P450 2C
3	29	31.5	12	PN0170	alcohol dehydrogen
4	28	30.4	21	S58431	phosphatidylinositol
5	26	28.3	17	S59481	hydroxyproline-ric
6	26	28.3	19	S74114	3-hydroxyacyl-CoA
7	26	28.3	22	A37043	ig light chain, po
8	25	27.2	22	S57386	transglutaminase
9	25	27.2	22	PO0597	Rattus norvegicus (Norway rat)
10	24	26.1	13	A60856	C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
11	24	26.1	15	B35319	C;Accession: S29817
12	24	26.1	15	A36315	R;Marie, S.; Rousset, F.; Crestein, T.
13	24	26.1	17	I76673	Biochim. Biophys. Acta 1172, 124-130, 1993
14	24	26.1	24	A24117	A;Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
15	24	26.1	24	S70129	A;Accession: S29817
16	24	26.1	24	S38729	A;Molecule type: mRNA
17	23	25.0	10	PN0165	A;Residues: 1-20 <MAR>
18	23	25.0	12	PN0663	C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
19	23	25.0	15	I46509	C;Keywords: heme; transmembrane protein
20	23	25.0	15	A56363	acid phosphatase (
21	23	25.0	16	S69161	carbamoyl-phosphat
22	23	25.0	18	PC2280	prolylendopeptidases
23	23	25.0	19	A32917	protein phosphatas
24	23	25.0	19	A47889	flagellar sheath P
25	23	25.0	22	S63674	28 k secretory pro
26	23	25.0	23	T44118	carbamoyl-phosphat
27	23	25.0	24	S08185	proteasome alpha c
28	23	25.0	24	S40139	T-cell receptor-J-
29	23	25.0	25	S00329	beta-N-acetylgluco

Query Match Best Local Similarity 39.1%; Score 36; DB 2; Length 18;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match Best Local Similarity 50.0%; Score 50.1%; DB 2; Length 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match Best Local Similarity 39.1%; Score 36; DB 2; Length 18;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match Best Local Similarity 50.0%; Score 50.1%; DB 2; Length 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match Best Local Similarity 39.1%; Score 36; DB 2; Length 18;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match Best Local Similarity 39.1%; Score 36; DB 2; Length 18;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Query Match Best Local Similarity 32.6%; Score 30; DB 2; Length 20;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match Best Local Similarity 32.6%; Score 30; DB 2; Length 20;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match Best Local Similarity 32.6%; Score 30; DB 2; Length 20;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Query Match Best Local Similarity 32.6%; Score 30; DB 2; Length 20;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
 PN0170 alcohol dehydrogenase (EC 1.1.1.1) - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 31-Jan-1997
 R;Fuksaya, N.; Chow, L.P.; Sugiyra, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994
 A;Reference number: PN0170
 A;Accession: PN0160
 A;Molecule type: protein
 A;Residues: 1-12 <DIE>
 A;Experimental source: strain M-1-1
 C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 31.5%; Score 29; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 83; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 LLKEFTVSG 16
 |||| :|| |
 Db 2 LLKGTVNDG 10

RESULT 4
 S58431 phosphatidylinositol transfer protein isoform, 36K - bovine
 C;Species: Bos primigenius taurinus (cattle)
 C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
 C;Accession: S58431
 C;De Vries, K.J.; Heinrichs, A.A.J.; Cunningham, E.; Brunink, F.; Westerman, J.; Somerha
 Biochem. J. 310, 643-649, 1995
 A;Title: An isoform of the phosphatidylinositol-transfer protein transfers sphingomyelin
 A;Reference number: S58430; MUID:95382786
 A;Accession: S58431
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-21 <DEV>
 C;Superfamily: human phosphatidylinositol transfer protein

Query Match 30.4%; Score 28; DB 2; Length 21;
 Best Local Similarity 75.0%; Pred. No. 2.3e+01; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 VLLKEFTV 14
 |||| :|
 Db 1 VLLKEFRV 8

RESULT 5
 S59481 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
 C;Species: Phaseolus vulgaris (kidney bean)
 C;Accession: S59481
 C;De: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
 R;Wojtaszek, P.; Treharne, J.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A;Title: Specificity in the immobilisation of cell wall proteins in response to different
 A;Reference number: S59481; MUID:96011753
 A;Accession: S59481
 A;Molecule type: protein
 A;Residues: 1-17 <WOD>
 C;Keywords: glycoprotein; hydroxyproline
 F; 6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 28.3%; Score 26; DB 2; Length 17;
 Best Local Similarity 41.7%; Pred. No. 4.1e+02; Indels 5; Mismatches 2; Gaps 0;

Qy 1 PLVPVGVLKEF 12
 || :| | :| :|
 Db 6 PVPPPPVYYPPTF 17

RESULT 6
 S74114 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: S74114
 R;Dieulaide-Noubhani, M.; Novikov, D.; Baumgart, E.; Vanhooren, J.C.T.; Fransen, M.; G
 Eur. J. Biochem. 240, 660-666, 1996
 A;Title: Further characterization of the peroxisomal 3-hydroxyacyl-CoA dehydrogenases
 e acids di- and tri-hydroxycoprostanic acids are metabolized by separate multifunctional
 A;Reference number: S74113; MUID:97008358
 A;Accession: S74114
 A;Molecule type: protein
 A;Residues: 1-19 <DIE>
 A;Experimental source: liver
 C;Superfamily: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA dehydrogenase homolog
 C;Keywords: fatty acid beta-oxidation; mitochondrion; NAD; Oxidoreductase

Query Match 28.3%; Score 26; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 VLLKEFTVSG 16
 || :| | :| |
 Db 4 ILIKHVTVIG 13

RESULT 7
 A37043 Ig light chain, polyclonal pool - elephantfish (Callorhynchus callorhynchus) (fragment)
 C;Species: Callorhynchus callorhynchus
 C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 16-Aug-1996
 C;Accession: A37043
 R;De Ioannes, A.E.; Aguila, H.L.
 Immunogenetics 30, 175-180, 1989
 A;Title: Amino terminal sequence of heavy and light chains from ratfish immunoglobuli
 A;Reference number: A37043; MUID:89379382
 A;Accession: A37043
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-22 <DEI>
 C;Keywords: immunoglobulin

Query Match 28.3%; Score 26; DB 2; Length 22;
 Best Local Similarity 62.5%; Pred. No. 5.4e+02; Indels 0; Gaps 0;

Qy 3 PVPGVLK 10
 |||| :|
 Db 12 PVPGNTVK 19

RESULT 8
 S57286 translation elongation factor aef-1 beta - Sulfolobus solfataricus (fragments)
 C;Species: Sulfolobus solfataricus
 C;Accession: S57286
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
 C;Arcari, P.; Raimo, G.; Ianniciello, G.; Gallo, M.; Bocchini, V.
 Biophys. Acta 1263, 86-98, 1995
 A;Title: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.
 A;Reference number: S57286
 A;Accession: S57286
 A;Status: preliminary
 A;Molecule type: protein

A; Residues: 1-20 <ARC>

Query Match Score 25; DB 2; Length 20;
 Best Local Similarity 27.2%; Pred. No. 7.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 VLKEFTVSG 16
 Db 5 WLKVFPVVG 14

RESULT 9

P00697 hemagglutinin [imported] - rice (fragment)
 C;Species: Oryza sativa (rice)

C;Accession: P00697
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A; Reference number: P00696

A; Accession: P00697

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-22 <ROM>

Query Match Score 25; DB 2; Length 22;

Best Local Similarity 27.2%; Pred. No. 8.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 11 EPTVSGNI 18

Db 3 KFVVCGNL 10

RESULT 10

A60856 inhibin alpha chain - sheep (fragment)

C;Species: Ovis orientalis aries Ovis ammon aries (domestic sheep)

C;Accession: A60856
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993

R;Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenthal, J.; Endocrinol. 113, 213-221, 1987

A;Title: Isolation of inhibin from ovine follicular fluid.

A; Reference number: A60856; MUID:97224684

A; Accession: A60856

A; Molecule type: protein

A; Residues: 1-13 <LEV>

C;Comment: Inhibin suppresses follicle-stimulating hormone secretion.

C;Superfamily: inhibin

C;Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match Score 24; DB 2; Length 13;

Best Local Similarity 26.1%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLPVPP 5

Db 4 PLPXP 8

RESULT 11

B35389 urease (EC 3.5.1.5) 15K chain - Morganella morganii (fragment)

C;Species: Morganella morganii

C;Accession: 31-Aug-1990 #sequence_revision 31-Aug-1990

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J;Bacteriol. 172, 3073-3080, 1990

A;Title: Morganella morganii urease: purification, characterization, and isolation of ge

A;Reference number: A35389; MUID:90264298

A;Accession: B35389
 A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <SHUA>

C;Keywords: hydrolase

Query Match Score 24; DB 2; Length 15;

Best Local Similarity 26.1%; Pred. No. 7.8e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PLPVPGVIL 8

Db 6 PTPLUGVIL 13

RESULT 12

A6315 recycling receptor p180 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991

C;Accession: A36315

R;Isacke, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.

Mol. Cell. Biol. 10, 2606-2618, 1990

A;Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type

A;Reference number: A36315; MUID:90258846

A;Accession: A36315

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <ISA>

Query Match Score 24; DB 2; Length 15;

Best Local Similarity 26.1%; Pred. No. 7.8e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LPVPGVLL 9

Db 1 1 1 1 1

Db 7 LPPEPNVFL 14

RESULT 13

I76673 hypothetical COII/ND5 mutant fusion protein - mouse mitochondrial (fragment)

N;Alternative names: COII/ND5 protein

C;Species: mitochondrial Mus musculus (house mouse)

C;Date: 12-Aug-1996 #sequence_revision 16-Jul-1998

C;Accession: I76673; I76674

R;Nelson, T.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.

Mamm. Genome 4, 680-683, 1993

A;Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic m

A;Reference number: I57011; MUID:94108239

A;Accession: I76673

A;Molecule type: DNA

A;Residues: 1-17 <NEL>

A;Cross references: GB:S68119; NID:9544777

A;Accession: I76674

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 8-17 <NEL>

A;Cross references: GB:S68119; NID:9544777

C;Comment: This is the hypothetical translation of a sequence believed to result from

C;Genetics:

A;Gene: COII/ND5

A;Genome: mitochondrial

A;Genetic code: SCG1

C;Keywords: fusion Protein; mitochondrial

F;1-7/Region: cytochrome-c oxidase chain II

R;Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.

J;Bacteriol. 172, 3073-3080, 1990

A;Title: Morganella morganii urease: purification, characterization, and isolation of ge

Query Match 26.1%; Score 24; DB 4; Length 17;
 Best Local Similarity 50.0%; Pred. No. 9e-02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
 C:Accession: A24417
 R;Pong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205 309-312, 1986
 A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A;Reference number: A91365; MUID:86301171
 A;Accession: A24417
 A;Molecule type: protein
 A;Residues: 1-24 <FON>
 C;Superfamily: interphotoreceptor retinoid-binding protein
 C;Keywords: duplication

Query Match 26.1%; Score 24; DB 2; Length 24;
 Best Local Similarity 35.3%; Pred. No. 1.3e+03;
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 C:Species: Secale cereale (rye)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 02-Jul-1998
 C:Accession: S70329
 R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
 Biochim. Biophys. Acta 1295, 13-22, 1996
 A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.
 A;Reference number: S70327; MUID:96283789
 A;Accession: S70329
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <ROC>
 C;Superfamily: gliadin

RESULT 14
 A24417
 interphotoreceptor retinoid-binding protein - sheep (fragment)
 C:Species: interstitial retinol-binding protein
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
 R;Pong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205 309-312, 1986
 A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A;Reference number: A91365; MUID:86301171
 A;Accession: A24417
 A;Molecule type: protein
 A;Residues: 1-24 <FON>
 C;Superfamily: interphotoreceptor retinoid-binding protein
 C;Keywords: duplication

Query Match 26.1%; Score 24; DB 2; Length 24;
 Best Local Similarity 35.3%; Pred. No. 1.3e+03;
 Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 C:Species: Secale cereale (rye)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 02-Jul-1998
 C:Accession: S70329
 R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
 Biochim. Biophys. Acta 1295, 13-22, 1996
 A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.
 A;Reference number: S70327; MUID:96283789
 A;Accession: S70329
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <ROC>
 C;Superfamily: gliadin

Query Match 26.1%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 C:Species: Secale cereale (rye)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 02-Jul-1998
 C:Accession: S70329
 R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
 Biochim. Biophys. Acta 1295, 13-22, 1996
 A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.
 A;Reference number: S70327; MUID:96283789
 A;Accession: S70329
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <ROC>
 C;Superfamily: gliadin

Scoring table:	BLOSUM62	Score:	34	20	21.7	23	1	GLMS_CLOC0
Gapop:	10.0	Gapext:	0.5	35	20	21.7	24	1 HEMT_LINRE
Searched:	93435 seqs., 34255486 residues	Total number of hits satisfying chosen parameters:	1423	36	20	21.7	24	1 LPER_STRFR
Minimum DB seq length:	0	Post-processing: Minimum Match	0%	37	20	21.7	25	1 LYC_ASTRV
Maximum DB seq length:	25	Maximum Match	100%	38	20	21.7	25	1 PATX_PARCV
Database :	SwissProt_39;*	Listing first 45 summaries		39	19	20.7	9	1 MGMT_BOVIN
Scoring table:	BLOSUM62	Score:	92	41	19	20.7	10	1 PAP1_PARM1
Gapop:	10.0	Gapext:	0.5	42	19	20.7	16	1 FOR2_MYRG1
Sequence:	1 PLPVPGVLLKEFTVSGNI 18	Post-processing: Maximum Match	100%	43	19	20.7	17	1 BOL4_MEGLP
		Listing first 45 summaries		44	19	20.7	17	1 NU4M_TRIUR
				45	19	20.7	20	1 UP24_UPETIN
								1 AROQ_AMYME
								1 P82030_uperoletia
								1 P46380_amycolatops
ALIGNMENTS								
RESULT	1	YCIA_SALTY	STANDARD;	PRT;	13 AA.			
ID	YCIA_SALTY							
AC	P25944;							
DT	01-MAY-1992 (Rel. 22, Created)							
DT	01-MAY-1992 (Rel. 22, Last sequence update)							
DT	01-OCT-2000 (Rel. 20, Last annotation update)							
DE	PUTATIVE ACYL-COA THIESTER HYDROLASE YCIA (EC 3.1.2.-) (P14 PROTEIN)							
DE	(FRAGMENT).							
GN								
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=9109409; PubMed=2266561;							
RA	Hannary K., Barr G.C., Dorman C.J., Mazengera L.R., Adamson J.,							
RA	Gallagher M.P., Evans J.S., Levine B.A., Trayer T.P., Higgins C.F.;							
RT	"TonB protein of <i>Salmonella typhimurium</i> . A model for signal transduction between membranes".							
RL	J. Mol. Biol. 216:897-910(1990).							
CC	-!- SIMILARITY: BELONGS TO THE ACYL COENZYME A HYDROLASE FAMILY.							
CC								
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration							
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -							
CC	the European Bioinformatics Institute. There are no restrictions on its							
CC	use by non-profit institutions as long as its content is in no way							
CC	modified and this statement is not removed. Usage by and for commercial							
CC	purposes requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).							
CC								
DR	X56434; :- NOT_ANNOTATED_CDS.							
DR	StyGene; SG10418; YCIA.							
KW	Hypothetical protein; Hydrolase.							
FT	Best Local Similarity 83.3%; Pred. No. 1.e+02;							
FT	NON_TER 1 1							
SQ	SEQUENCE 13 AA: 1307 MN; 30960DC5EFAC7417 CRC64;							
QY	1 PLPVPG 6							
QY								
Db	8 PLPVQG 13							
RESULT	2	UC29_MAIZE	STANDARD;	PRT;	15 AA.			
ID	UC29_MAIZE							
AC	P80635;							
DT	01-OCT-1996 (Rel. 34, Created)							
DT	01-OCT-1996 (Rel. 34, Last sequence update)							
DT	15-JUL-1999 (Rel. 38, Last annotation update)							
DE	UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 45)							

DE (FRAGMENT).	ID DHAG_COMTE STANDARD; PRT; 24 AA.
OS Zea mays (Maize); Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	AC P80705; 01-OCT-1996 (Rel. 34, Created)
OC Eukaryota; Liopsida; Poales; Poaceae; PACC clade; Panicoideae;	DT 01-OCT-1996 (Rel. 34, Last sequence update)
OC Andropogonaceae; Zea.	DT 15-DEC-1998 (Rel. 37, Last annotation update)
OX NCBI_TaxID=4577;	DE ALDHYDE DEHYDROGENASE, GAMMA CHAIN (EC 1.2.90.3) (ALDH) (FRAGMENT).
RN [1]	OS Comamonas testosteroni (Pseudomonas testosteroni).
RP Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.	OC NCBITaxID=285;
RC TISSUE-Coleoptile;	OX RN [1]
RA Perronnet J.-C., Riccardi F., Morin C., Dannerval C., Huet J.-C.,	RP SEQUENCE.
RT "The maize two dimensional gel protein database: towards an integrated	RC STRAIN=ATCC 15667;
RT genome analysis program.";	RA Luykx D.M.A.M., Kim S.W., de Vries S., Duine J.A.;
RL Theor. Appl. Genet. 93:997-1005(1996).	RL Submitted (JUN-1996) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN	CC -!- CATALYTIC ACTIVITY: AN ALDEHYDE + ACCEPTOR + H(2)O = AN ACID +
CC Maize-DBPAGE: P80635; COLIOPITTLE.	CC -!- COFACTOR: MOLYBDENUM.
DR Maizedb: 123960; -	CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA
FT NON_TER 1 1	CC CHAIN.
FT NON_TER 15 15	KW Oxidoreductase; Molybdenum.
SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;	FT NON_TER 24 24 AA; 2585 MW; 9E66B518130EA938 CRC64;
SQ	SEQUENCE 24 AA; 2585 MW; 9E66B518130EA938 CRC64;
Query Match 27.2%; Score 25; DB 1; Length 15;	Query Match 26.1%; Score 24; DB 1; Length 24;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;	Best Local Similarity 66.7%; Pred. No. 7.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PLVP 5	Qy 11 EFTVSG 16
Db 4 PPIP 8	Db 4 QFTVNG 9
RESULT 3	RESULT 5
URB2_MORMO STANDARD; PRT; 15 AA.	IRBP_SHEEP STANDARD; PRT; 24 AA.
AC P17338;	AC P12663;
DT 01-AUG-1990 (Rel. 15, Last sequence update)	DT 01-OCT-1989 (Rel. 12, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)	DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)	DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE UREASE BETA SUBUNIT (EC 3.5.1.5) (15 KDa SUBUNIT) (UREA AMIDOHYDROLASE) (FRAGMENT).	DE INTERPHOTORECEPTOR RETINOID-BINDING PROTEIN (IRBP) (INTERSTITIAL DE RETINOL-BINDING PROTEIN) (FRAGMENT).
GN UREB.	GN RBP3.
OS Morganella morganii (Proteus morganii)	OS Ovis aries (Sheep).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
OC Morganella	OC Bovidae; Caprinae; Ovis.
RN [1]	OX NCBITaxID=9440;
RP SEQUENCE.	RN [1]
RX MEDLINE=90264298; PubMed=2345135;	RP SEQUENCE.
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.,	RX MEDLINE=86301171; PubMed=3743780;
RT "Morganella morganii urease: purification, characterization, and isolation of gene sequences";	RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A., Bridges C.D.B.;
RL J. Bacteriol. 173:3073-3080(1990).	RA "N-terminal sequence homologies in interstitial retinol-binding proteins from 10 vertebrate species.";
CC -!- CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3).	RT FEBS Lett. 205:309-312(1986).
CC -!- SIMILARITY: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).	CC -!- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
DR PIR; B35389; B35389.	CC -!- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT CC EPITHELIUM CELLS.
KW Hydrolyase.	DR PIR; A24417; A24417.
FT NON_TER 15 15	KW Vitamin A; transport.
SEQUENCE 15 AA; 1530 MW; 2D98944F2F20C7E8 CRC64;	FT NON_TER 24 24 AA; 2799 MW; 02EDBE61A8E4523 CRC64;
SQ	Query Match 26.1%; Score 24; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;	Best Local Similarity 35.3%; Pred. No. 7.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 1 PLVPGVY 8	Qy 2 LPVPGVYIKEFTVSGNI 18
Db 6 PTPLGGVY 13	
RESULT 4	
DHAG_COMTE	

Db	Query	Best Local Similarity	Matches	5; Conservative	1; Mismatches	2; Indels	0; Gaps	0;
6	1 : : 7 LDMAQVLLDNYYTTPENL 23	25.0%; Score 23; DB 1; Length 13;	Qy	2 LPVPGVLL 9				
CRBL_VESNA	STANDARD;	PRT; 13 AA.	Db	2 LPIVGNIL 9				
AC P17332;			RESULT 8					
DT 01-AUG-1990 (Rel. 15, Created)	COG4_CHIOP	STANDARD;	ID COG4_CHIOP					
DT 01-DEC-1998 (Rel. 37, Last annotation update)	AC P34156;	PRT; 20 AA.	ID P34156;					
DE VESPID CHEMOPACTIC PEPTIDE M (VESCP-M).	DT 01-FEB-1994 (Rel. 28, Created)		AC P34156;					
OS Vespa mandarina (Hornet).	DT 01-FEB-1994 (Rel. 28, Last sequence update)		DT 01-FEB-1994 (Rel. 32, Last annotation update)					
CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.	DT 01-NOV-1995 (Rel. 32, Last annotation update)		DT 01-NOV-1995 (Rel. 32, Last annotation update)					
CC KW Mast cell degranulation; Chemotaxis; Venom; Amidation.	DE COLLAGENOLYTIC PROTEASE 23 KDA (EC 3.4.24.7) (FRAGMENT).		DE COLLAGENOLYTIC PROTEASE 23 KDA (EC 3.4.24.7) (FRAGMENT).					
FT MOD RES 13	OS Chioneocetes opilio (Crab-beetle).		OS Chioneocetes opilio (Crab-beetle).					
SEQUENCE: 13 AA; 1384 MW;	OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Bivalacostraca; Bucardiida; Decapoda; Pleocyemata; Brachyura; Subbrachyura; Maloidea; Majidae; Chionoecetes.		OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Bivalacostraca; Bucardiida; Decapoda; Pleocyemata; Brachyura; Subbrachyura; Maloidea; Majidae; Chionoecetes.					
RN NCBI_TaxID=7446;	OX NCBI_TaxID=41210;		OX NCBI_TaxID=41210;					
RP TISSUE="venom";	RN [1]		RN SEQUENCE.					
RA Fujino M.;	RP TISSUE=Hepatopancreas;		RC MEDLINE=9212007;					
(In) Muneoka E. (eds.);	RC MEDLINE=9212007;		RC Published=1663026;					
RL Peptide Chemistry 1983, pp.185-190, Protein Research Foundation,	RA Klimova O.A., vedishcheva Y.V., Strongin A.Y.		RA					
RL (1984).	CC "Isolation and characteristics of collagenolytic enzymes from the hepatopancreas of the crab Chioneocetes opilio."		CC					
CC -!- FUNCTION: THIS ENZYME IS A METAL PROTEASE CAPABLE OF DEGRADING THE NATIVE TRIPLE HELIX OF COLLAGEN.	FT DR		FT DR					
CC -!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).	CC DR		CC DR					
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.	CC DR		CC DR					
CC HSSP; P07504; ITAD.	CC DR		CC DR					
CC MEROPS; M12.001; -;	CC DR		CC DR					
CC Interpro; IPR00130; -;	CC DR		CC DR					
CC PROSITE; PS00142; ZINC PROTEASE; PARTIAL.	CC DR		CC DR					
CC Hydrolase; Metalloprotease; Zinc; Collagen degradation.	CC DR		CC DR					
FT NON-TER 20	FT NON-TER 20		FT NON-TER 20					
SQ SEQUENCE 20 AA; 2108 MW;	SQ SEQUENCE 20 AA; 2108 MW;		SQ SEQUENCE 20 AA; 2108 MW;					
RESULT 7	Query Match 25.0%; Score 23; DB 1; Length 20;		Query Match 25.0%; Score 23; DB 1; Length 20;					
TEM_PANTE	Best Local Similarity 33.38%; Pred. No. 8.8e+02;		Best Local Similarity 33.38%; Pred. No. 8.8e+02;					
AC P56919;	Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;		Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;					
DT 30-MAY-2000 (Rel. 39, Created)	AC P56918;		AC P56918;					
DT 01-OCT-2000 (Rel. 40, Last sequence update)	DT 30-MAY-2000 (Rel. 39, Created)		DT 30-MAY-2000 (Rel. 39, Created)					
DT 01-OCT-2000 (Rel. 40, Last annotation update)	DT 01-OCT-2000 (Rel. 40, Last sequence update)		DT 01-OCT-2000 (Rel. 40, Last annotation update)					
DE TEMPORIN D.	DE TEMPORIN C.		DE TEMPORIN C.					
OS Rana temporaria (European common frog).	OS Rana temporaria (European common frog).		OS Rana temporaria (European common frog).					
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.	CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.		CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.					
OX NCBI_TaxID=8407;	OX NCBI_TaxID=8407;		OX NCBI_TaxID=8407;					
RN SEQUENCE, AND SYNTHESIS.	RN SEQUENCE, AND SYNTHESIS.		RN SEQUENCE.					
RC TISSUE="Skin";	RC TISSUE="Skin";		RC TISSUE="Skin";					
RX MEDLINE=97175050; PubMed=9022710;	RX MEDLINE=97175050; PubMed=9022710;		RX MEDLINE=97175050; PubMed=9022710;					
RA Simmaco M., Mignogna G., canofeni S., Miele R., Mangoni M.L., Barra D.;	RA Simmaco M., Mignogna G., canofeni S., Miele R., Mangoni M.L., Barra D.;		RA Simmaco M., Mignogna G., canofeni S., Miele R., Mangoni M.L., Barra D.;					
RT "Temporins", antimicrobial peptides from the European red frog Rana temporaria."	RT "Temporins", antimicrobial peptides from the European red frog Rana temporaria."		RT "Temporins", antimicrobial peptides from the European red frog Rana temporaria."					
RL Eur. J. Biochem. 242:788-792(1996).	RL Eur. J. Biochem. 242:788-792(1996).		RL Eur. J. Biochem. 242:788-792(1996).					
CC -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.	CC -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.		CC -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.					
CC -!- SUBCELLULAR LOCATION: SECRETED.	CC -!- SUBCELLULAR LOCATION: SECRETED.		CC -!- SUBCELLULAR LOCATION: SECRETED.					
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.	CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.		CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN FAMILY.					
KW Amphibian skin; Amidation; Multigene family.	KW Amphibian skin; Amidation; Multigene family.		KW Amphibian skin; Amidation; Multigene family.					
FT MOD RES 13	FT MOD RES 13		FT MOD RES 13					
SEQUENCE 13 AA;	SEQUENCE 13 AA;		SEQUENCE 13 AA;					
OX 3EF35DFA55B2448 CRC64;	OX 3EF35DFA55B2448 CRC64;		OX 3EF35DFA55B2448 CRC64;					
Query Match 25.0%; Score 23; DB 1; Length 13;	Query Match 25.0%; Score 23; DB 1; Length 13;		Query Match 25.0%; Score 23; DB 1; Length 13;					
Best Local Similarity 62.5%; Pred. No. 5.5e+02;	Best Local Similarity 62.5%; Pred. No. 5.5e+02;		Best Local Similarity 62.5%; Pred. No. 5.5e+02;					

CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Amphibian skin; Antibiotic; Amidation; Multigene family.
 FT MOD_RES 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1363 MW; 2201403A65B2448 CRC64;

Query Match Similarity 23.9%; Score 22; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LPVPGVLL 9
 ||: |||
 Db 2 LPFLGNL 9

RESULT 10
 TME_RANTE ID TEME_RANTE STANDARD; PRT; 13 AA.
 AC P56920;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE TEMPORINE.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=9715050; PubMed=302210;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT antimicrobial peptides from the European red frog Rana
 temporaria.;"
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 CC BACTERIA.
 CC -!- SUBCELLULAR LOCATION: SECRETED.

CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KW Amphibian skin; Antibiotic; Amidation; Multigene family.
 FT MOD_RES 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;

Query Match Similarity 23.9%; Score 22; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LPVPGVLL 9
 ||: |||
 Db 2 LPFLGNL 9

RX MEDLINE=95188911; PubMed=7883009;
 RA Bytemans D., Froost P., Samijn B., Borovsky D., Grauwels L.,
 RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
 RT "Neb-colloostatin, a second follliculostatin of the grey fleshfly,
 Neobellleria bullata."
 RL Eur. J. Biochem. 228:45-49(1995).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
 CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PRETELLOGENIC
 CC FOLLICLES.
 CC -!- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
 CC -!- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
 CC COLLAGEN IV.
 SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5FOCEBB8251 CRC64;

Query Match Similarity 23.9%; Score 22; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LPVP 5
 |||||
 Db 7 LPVP 10

RESULT 12
 KORA_METTM ID KORA_METTM STANDARD; PRT;
 AC P80304;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 2-OXOGLUTARATE SYNTHASE SUBUNIT KORA (EC 1.2.7.3) (2-KETOGLUTARATE
 DE OXIDOREDUCTASE ALPHA CHAIN) (KOR) (2-OXOGLUTARATE-FERRDOXIN
 DE OXIDOREDUCTASE ALPHA SUBUNIT) (FRAGMENT).
 GN KORA.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Eurarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanothermobacter.
 NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97261844; PubMed=9108258;
 RA Terpstraen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
 in Methanobacterium thermoautotrophicum.";
 RL Eur. J. Biochem. 244:867-880(1997).
 CC -!- CATALYTIC ACTIVITY: 2-OXBUTANOATE + COA + OXIDIZED FERREDOXIN =
 CC PROPAONOYL-COA + CO(2) + REDUCED FERREDOXIN.
 CC -!- SUBUNIT: HETEROTETRAMER OF THE KORA, KORB, KORC AND KORD
 CC SUBUNITS.
 CC -!- TEMPERATURE IS 70 DEGREES CELSIUS.
 CC KW Oxidoreductase.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2080 MW; 112E7E0E4AC76B76 CRC64;

Query Match Similarity 23.9%; Score 22; DB 1; Length 20;
 Best Local Similarity 37.5%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 10 KEFVSGN 17
 ||: |||
 Db 2 EEYFIQGN 9

RESULT 13
 LPR_BACT ID LPR_BACT STANDARD; PRT;
 AC P0558;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE.

TETRACYCLINE RESISTANCE LEADER PEPTIDE.

DE TETRL.
 GN Bacillus stearothermophilus, *Bacillus cereus*, and
Staphylococcus *hyicus*.
 OS Plasmid pBCT15; Plasmid PBC16, and Plasmid pSTE1.
 OC Bacteria; Firmicutes; *Bacillus/Clostridium* group;
Bacillus/Staphylococcus group; *Bacillus*.
 NCBI_TaxID=1422, 1396, 1284.

RN [1] SEQUENCE FROM N.A.
 RP PLASMID=pBCT15;
 RX MEDLINE=86031344; PubMed=2996983;

RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pBCT15, a
 thermophilic *Bacillus* plasmid: comparison with staphylococcal TCR
 controls.";
 RL Gene 37:131-138(1985).

RN [2] SEQUENCE FROM N.A.
 RP PLASMID=pBCT16;
 RX MEDLINE=90221899; PubMed=2109312;

RA Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pBCT16
 from *Bacillus cereus*";
Nucleic Acids Res. 18:1635-1635(1990).

RN [3] SEQUENCE FROM N.A.
 RP PLASMID=pSTE1;
 RX MEDLINE=92321725; PubMed=1622166;

RA Schwartz S., Cardoso M., Wegener H.C.;
 RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline
 resistance determinant encoded by plasmid pSTE1 from *Staphylococcus*
hyicus";
 RL *Antimicrob. Agents Chemother.* 36:580-588(1992).

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 DR EMBL; D00006; BAA00004..1; ..
 DR EMBL; M11036; AAA22850..1; ..
 DR EMBL; X60828; CAA43219..1; ..
 DR PIR; S09233; LFBSTU.
 DR PIR; S23742; S23742.

KW Leader peptide; Antibiotic resistance; Plasmid.
 SQ SEQUENCE 20 AA; 2253 MW; 18D0FA6CA231CA1 CRC64;

Query Match 23.9%; Score 22; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Gaps 0;

Qy 7 VLKEFVSV 15
 Db 9 VQLREGSVS 17

RESULT 14
 LPTR_BACSU STANDARD; PRT; 20 AA.
 ID LPTR_BACSU STANDARD; PRT; 20 AA.
 AC P23053;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE TETRL.
 GN TETL.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; *Bacillus/Clostridium* group;

OC *Bacillus/Staphylococcus* group; *Bacillus*.
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=168;
 RX MEDLINE=89000797; PubMed=2844262;
 RA Salaguchi R., Amano H., Shishido K.;
 RT "Nucleotide sequence homology of the tetracycline-resistance
 determinant naturally maintained in *Bacillus subtilis* Marburg
 chromosome and the tetracycline-resistance gene of *B. subtilis*
 plasmid pNS1981";
 RL *Biochim. Biophys. Acta* 950:441-444(1988).
 RN [2] SEQUENCE FROM N.A.
 RP MEDLINE=91257555; PubMed=1646143;
 RA Amano H., Salaguchi R., Shishido K.;
 RT "An insertion of *Escherichia coli* transposable element IS1K into the
 site immediately before tetracycline-resistance determinant of
Bacillus subtilis chromosome DNA fragment in cloning in *E. coli*.";
 RL *PEMS Microbiol. Lett.* 63:5-8(1991).
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 CC
 DR EMBL; X08034; CAA30826..1; ..
 DR EMBL; X58999; CAA1744..1; ..
 DR EMBL; Z99124; CAB1615..1; ..
 PIR; S04802; LFBSTU.
 DR S17282; S17282.
 DR SubList; BG11051; tETL.
 DR Leader peptide; Antibiotic resistance.
 SQ SEQUENCE 20 AA; 2298 MW; E870F516CA23111A CRC64;

Query Match 23.9%; Score 22; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 VLKEFVSV 15
 Db 9 VQLREGSVS 17

RESULT 15
 TNB_ACTTE STANDARD; PRT; 20 AA.
 ID TNB_ACTTE AC P31034;
 AC P31034;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TENEBROSIN B (FRAGMENT).
 OS *Actinia tenebrosa* (Australian red waratah sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nyantheae; Actiniidae; Actinia.
 RN (1)

RP SEQUENCE.
 RX MEDLINE=90232538; PubMed=1970442;
 RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
 RA Moritz R.L., Simpson R.J.;
 RT "Purification and characterisation of proteins with cardiac
 stimulatory and haemolytic activity from the anemone *Actinia*
tenebrosa";
 RT Toxicon 28:20-41(1990).
 CC -1- FUNCTION: THIS CARDIAC STIMULATORY AND HEMOLYTIC PROTEIN IS A
 CC CHANNEL-FORMING AND/OR MEMBRANE-PENETRATING PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE TENEBROSIN FAMILY.
 DR PIR; B34016; B34016.

KW Hemolysin; Toxin; Transmembrane.
FT 20
NON_TER 20
SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 23.9%; Score 22; DB 1; Length 20;
Best Local Similarity 26.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
Qy 4 VPOVLLKEFTVSSNI 18
| | :: | : | : | :
Db 4 VAGAVIETGATLIFNV 18

Search completed: May 8, 2001, 15:14:08
Job time: 529 sec

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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:16:06 : Search time 114.89 Seconds
(without alignments)
18.363 Million cell updates/sec

Title: US-09-165-546A-10
Perfect score: 92
Sequence: 1 PLPVPGVLLKEFTYSGNI 18

Scoring table: BIOJUN62
Gapop 10.0 , Gapext. 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```
SPTRMBL_15;*
1: sp_archaea;*
2: sp_bacteria;*
3: sp_fungi;*
4: sp_human;*
5: sp_invertebrate;*
6: sp_mammal;*
7: sp_mhc;*
8: sp_organelle;*
9: sp_phage;*
10: sp_plant;*
11: sp_rabbit;*
12: sp_unclassified;*
13: sp_vertebrate;*
14: sp_virus;*
```

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query	Match	Length	DB	ID	Description
1	30	32.6	20	11	Q9QW31		Q9qw31 rattus sp.
2	29	31.5	21	6	09TR36		09tr36 bos taurus
3	29	31.5	22	2	09ZAW2		09zaw2 francisella
4	29	31.5	24	2	052390		052390 nodularia s
5	28	30.4	21	6	09TR37		09tr37 bos taurus
6	28	30.4	24	4	09UCP1		09ucp1 homo sapien
7	28	30.4	24	11	Q9QVC8		09qvc8 rattus sp.
8	27.5	29.9	20	6	09TR55		09tr55 streptococcus
9	27.5	29.9	24	2	Q9R558		09r558 streptococc
10	27	29.3	18	6	P79214		P79214 orctoiaquus
11	25	27.2	15	4	09UCC2		09ucc2 homo sapien
12	25	27.2	16	2	Q47605		Q47605 escherichia
13	25	27.2	17	4	09UCB9		09ucb9 homo sapien
14	25	27.2	21	9	Q9T167		Q9t167 bacteriophaga
15	25	27.2	25	10	049883		049883 lycopersico
16	24	26.1	20	2	Q9R502		Q9r502 thermomoga
17	24	26.1	21	3	Q9UR89		Q9ur89 coelioide
18	24	26.1	21	11	Q9Z167		Q9z167 mus musculus
19	24	26.1	23	11	Q9Z208		Q9z208 mus musculus

ALIGNMENTS

RESULT	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3100	3200	3300	3400	3500	3600	3700	3800	3900	4000	4100	4200	4300	4400	4500	4600	4700	4800	4900	5000	5100	5200	5300	5400	5500	5600	5700	5800	5900	6000	6100	6200	6300	6400	6500	6600	6700	6800	6900	7000	7100	7200	7300	7400	7500	7600	7700	7800	7900	8000	8100	8200	8300	8400	8500	8600	8700	8800	8900	9000	9100	9200	9300	9400	9500	9600	9700	9800	9900	10000	10100	10200	10300	10400	10500	10600	10700	10800	10900	11000	11100	11200	11300	11400	11500	11600	11700	11800	11900	12000	12100	12200	12300	12400	12500	12600	12700	12800	12900	13000	13100	13200	13300	13400	13500	13600	13700	13800	13900	14000	14100	14200	14300	14400	14500	14600	14700	14800	14900	15000	15100	15200	15300	15400	15500	15600	15700	15800	15900	16000	16100	16200	16300	16400	16500	16600	16700	16800	16900	17000	17100	17200	17300	17400	17500	17600	17700	17800	17900	18000	18100	18200	18300	18400	18500	18600	18700	18800	18900	19000	19100	19200	19300	19400	19500	19600	19700	19800	19900	20000	20100	20200	20300	20400	20500	20600	20700	20800	20900	21000	21100	21200	21300	21400	21500	21600	21700	21800	21900	22000	22100	22200	22300	22400	22500	22600	22700	22800	22900	23000	23100	23200	23300	23400	23500	23600	23700	23800	23900	24000	24100	24200	24300	24400	24500	24600	24700	24800	24900	25000	25100	25200	25300	25400	25500	25600	25700	25800	25900	26000	26100	26200	26300	26400	26500	26600	26700	26800	26900	27000	27100	27200	27300	27400	27500	27600	27700	27800	27900	28000	28100	28200	28300	28400	28500	28600	28700	28800	28900	29000	29100	29200	29300	29400	29500	29600	29700	29800	29900	30000	31000	32000	33000	34000	35000	36000	37000	38000	39000	40000	41000	42000	43000	44000	45000	46000	47000	48000	49000	50000	51000	52000	53000	54000	55000	56000	57000	58000	59000	60000	61000	62000	63000	64000	65000	66000	67000	68000	69000	70000	71000	72000	73000	74000	75000	76000	77000	78000	79000	80000	81000	82000	83000	84000	85000	86000	87000	88000	89000	90000	91000	92000	93000	94000	95000	96000	97000	98000	99000	100000	101000	102000	103000	104000	105000	106000	107000	108000	109000	110000	111000	112000	113000	114000	115000	116000	117000	118000	119000	120000	121000	122000	123000	124000	125000	126000	127000	128000	129000	130000	131000	132000	133000	134000	135000	136000	137000	138000	139000	140000	141000	142000	143000	144000	145000	146000	147000	148000	149000	150000	151000	152000	153000	154000	155000	156000	157000	158000	159000	160000	161000	162000	163000	164000	165000	166000	167000	168000	169000	170000	171000	172000	173000	174000	175000	176000	177000	178000	179000	180000	181000	182000	183000	184000	185000	186000	187000	1

OX NCBI_TaxID=9913;	RA Shi L., Carmichael W.W.;
RN [1]	RT "ppi-cyano2, a protein serine/threonine phosphatase 1 gene from the cyanobacterium Microcystis aeruginosa UTEX 2063.";
RP	RT
SEQUENCE	RT
MEDLINE=95302786; Published=7654206;	DR Arch. Microbiol. 168:528-531(1997).
RX de Vries K.J., Heinrichs A.A., Cunningham E., Brunink F.,	DR EMBL: AF037161; AAC46049.1; -.
RA Cunningham E., Brunink F., Cockcroft S., Wirth K.W., Snoek G.T.;	DR INTERPRO; IPR000934; -.
RA "An isoform of the phosphatidylinositol-transfer protein transfers sphingomyelin and is associated with the Golgi system.";	DR PFAM; PF00149; STphosphatase; 1.
RT	FT NON_TER
RT	FT NON_TER
RL Biochem. J. 310:643-649(1995).	FT NON_TER
DR INTERPRO; IPR001666; -.	FT NON_TER
DR PF02121; IP_trans; 1.	FT NON_TER
DR PF02121; IP_trans; 1.	FT NON_TER
SQ SEQUENCE 21 AA; 2442 MW; 0978BC2B0067EFOE CRC64;	SO SEQUENCE 24 AA; 2768 MW; DB9C36D51C0DA51D CRC64;
Query Match 31.5%; Score 29; DB 6; Length 21;	Query Match 31.5%; Score 29; DB 2; Length 24;
Best Local Similarity 75.0%; Pred. No. 3.e+02;	Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 7 VLIKEFTV 14	Qy 8 LLKEFTVSGN 17
: :	:
Db 1 VLIKEFRV 8	Db 5 LIKLEFEVGGN 14
RESULT 3	RESULT 5
Q9ZAW2 PRELIMINARY; PRT; 22 AA.	Q9TR37 PRELIMINARY; PRT; 21 AA.
ID Q9ZAW2	ID Q9TR37
AC Q9ZAW2_	AC Q9TR37;
DT 01-MAY-1999 (TREMBLrel. 10, Created)	DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)	DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)	DE PHOSPHATIDYLINOSITOL-TRANSFER PROTEIN 35 KDa ISOFORM (FRAGMENT).
DE OS Bos taurus (Bovine).	OS
ENVA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.	OC
GN Francisellal tularensis.	OC
OS Francisellal tularensis.	OC
QC Bacteria; Proteobacteria; gamma subdivision; Francisella group; Francisellaceae.	OX NCBI_TaxID=9913;
OC NCBI_TaxID=263;	RN [1]
OX	RP
RN SEQUENCE FROM N.A.	RX MEDLINE=95382786; PubMed=7654206;
RC STRAIN=LVS (LIVE VACCINE STRAIN);	RA de Vries K.J., Heinrichs A.A., Cunningham E., Brunink F.,
RA CLAIROLIN H., Clairolin H., Boissinot M.;	RA Westerman J., Somerharju P.J., Cockcroft S., Wirtz K.W., Snoek G.T.;
RT "Cloning and characterization of Francisella tularensis LVS homolog of the E. coli cell division gene ftsZ.";	RA "An isoform of the phosphatidylinositol-transfer protein transfers sphingomyelin and is associated with the Golgi system.";
RT Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.	RL Biochem. J. 310:643-649(1995).
DR EMBL: U76309; AAC95559.1; -.	DR INTERPRO; IPR001666; -.
FT NON_TER 22	DR PF02121; IP_trans; 1.
FT SEQENCE 22 AA; 2333 MW; ADA9026DE208C0A5 CRC64;	SO SEQUENCE 21 AA; 2462 MW; EA5A50C9DA8CAF2D6 CRC64;
Query Match 31.5%; Score 29; DB 2; Length 22;	Query Match 30.4%; Score 28; DB 6; Length 21;
Best Local Similarity 55.6%; Pred. No. 3.8e+02;	Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 8 LLKEFTVSG 16	Qy 7 VLIKEFTV 14
: :	: :
Db 6 IAKEFSVTG 14	Db 1 VLIKEYRV 8
RESULT 4	RESULT 6
Q9UCP1 PRELIMINARY; PRT; 24 AA.	Q9UCP1 PRELIMINARY; PRT; 24 AA.
ID 052390	ID Q9UCP1
AC Q9UCP1;	AC Q9UCP1;
DT 01-JUN-1998 (TREMBLrel. 06, Created)	DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE SERINE/THREONINE PHOSPHATASE 2B (FRAGMENT).	DE FBKB59=59 KDa IMMUNOPHILIN.
GN PP2B-CYANO1.	OS Homo sapiens (Human).
OS Nodularia spumigena.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=70799;	OX NCBI_TaxID=9606;
RN [1]	RN [1]
RP	RP
SEQUENCE FROM N.A.	RX MEDLINE=92285692; PubMed=1376003;
RC STRAIN=L575;	RA Tai P.K., Albers M.W., Chang H., Faber L.E., Schreiber S.L.;
MEDLINE=98047369; PubMed=9385145;	RT "Association of a 59-kilodalton immunophilin with the glucocorticoid

RT receptor complex.";	DB	6 LEEF-VSGNL 14
RL Science 256:1315-1318(1992). SEQUENCE 24 AA; 2486 MW; 7BCF45D0AEE6EF736 CRC64;	SQ	
Query Match Score 28; DB 4; Length 24; Best Local Similarity 71.4%; Pred. No. 6.2e+02; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
Qy 1 PLPVPGV 7 : Db 16 PLPMEGV 22		
RESULT 7 Q9QVC8 PRELIMINARY; ID Q9QVC8 AC Q9QVC8; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update) DE FKBPS9=59 KDA IMMUNOPHILIN. OS Rattus sp. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; OC NCBI_TaxID=10118; RN [1] RP SEQUENCE. RX MEDLINE=9285652; PubMed=1376003; RA Tai P.K.; Albers M.W.; Chang H.; Faber L.E.; Schreiber S.L.; RT "Association of a 59-kilodalton immunophilin with the glucocorticoid receptor complex."; RL Science 256:1315-1318(1992). SQ SEQUENCE 24 AA; 2478 MW; 901A4B67B2AF5D16 CRC64;		
Query Match Score 28; DB 11; Length 24; Best Local Similarity 71.4%; Pred. No. 6.2e+02; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
Qy 1 PLPVPGV 7 : Db 16 PLPLQGV 22		
RESULT 8 Q9TRU5 PRELIMINARY; ID Q9TRU5 AC Q9TRU5; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update) DE FACTOR IX LIGHT CHAIN (GLA DOMAIN). OS Oryctolagus cuniculus (Rabbit). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986; RN [1] RP SEQUENCE. RX MEDLINE=2132840; PubMed=1776139; RA Rao L.V.; Hoang A.D.; RT "Purification and characterization of rabbit factor IX and its existence as a two-chain factor IX alpha in circulating plasma."; RL Thromb. Res. 64:57-68(1991). SQ SEQUENCE 20 AA; 2317 MW; 9368E94B44BF5800 CRC64;		
Query Match Score 27.5; DB 6; Length 20; Best Local Similarity 70.0%; Pred. No. 6.1e+02; Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;		
Qy 9 LKEFTVSGNL 18	SQ	
RESULT 9 Q9R558 PRELIMINARY; ID Q9R558 AC Q9R558; DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update) DE SUPERANTIGEN (FRAGMENT). OS Streptococcus pyogenes. OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus. OX NCBI_TaxID=1314; RN [1] RP SEQUENCE. RX MEDLINE=93352815; PubMed=8349810; RA Mollick J.A.; Miller G.G.; Musser J.M.; Cook R.G.; Grossman D.; Rich R.R.; RT "A novel superantigen isolated from pathogenic strains of Streptococcus pyogenes with aminoterminal homology to staphylococcal enterotoxins B and C"; RR HSSP; P34071; 1STE; RL J. Clin. Invest. 92:710-719(1993). SQ SEQUENCE 24 AA; 2563 MW; 7AB3BC2BA3A180B6 CRC64;		
Query Match Score 27.5; DB 2; Length 24; Best Local Similarity 47.6%; Pred. No. 7.8e+02; Matches 10; Conservative 2; Mismatches 6; Indels 3; Gaps 2;		
Qy 1 PLPVPGVLLK-EFT-VSGNL 18 : : : : Db 4 PDPTEPEOLNKSSQFTGVGMGNL 24		
RESULT 10 P79214 PRELIMINARY; ID P79214 AC P79214; DT 01-MAY-1997 (TREMBLrel. 03, Created) DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update) DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update) DE CFTR PROTEIN. GN CFTR. OS Oryctolagus cuniculus (Rabbit). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986; RN [1] SEQUENCE FROM N. A. RA Vuillamier S.; Denamur E.; RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases. DR EMBL; X95931; CA65172-1; SQ SEQUENCE 18 AA; 2050 MW; 4DIC55056C1CE1B5 CRC64;		
Query Match Score 27; DB 6; Length 18; Best Local Similarity 58.3%; Pred. No. 6.6e+02; Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;		
Qy 1 PLPVPGVLLKEF 12 : : : Db 5 PLEKAGVLSKL 16		
RESULT 11 Q9UCC2 PRELIMINARY; ID Q9UCC2 AC Q9UCC2; DT 01-MAY-2000 (TREMBLrel. 13, Created)		

DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		[1]
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)		
OS	35	KDA HEPARIN-RELEASEABLE PROTEIN (FRAGMENT).		
OS	Homo sapiens (Human)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TAXID:9606;			
RN				
RP	SEQUENCE.			
RX	Medline=94059921; PubMed=8241100;			
RA	Novotny W.F., Maffei T., Mehta R.L., Milner P.G.i.			
PT	"Identification of novel heparin-releasable proteins, as well as the			
RT	cytokines midkine and pleiotrophin, in human postheparin plasma. ";			
RL	Arterioscler. Thromb. 13:1798-1805(1993).			
SEQUENCE	15 AA; 1434 MW; 0585FFEE4FE8FF6265 CRC64;			
SQ				
Qy	1 PLPVPG 5		RESULT 14	
Db	5 PVPPIP 9		Q9r167 ID Q9r167 PRELIMINARY; PRT; 21 AA.	
RESULT 12			Q9r167 AC 01-MAY-2000 (TREMBLrel. 13, Created)	
Q47605	047605 PRELIMINARY; PRT; 16 AA.		01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
ID	047605; 01-NOV-1996 (TREMBLrel. 01, Created)		01-JUN-2000 (TREMBLrel. 14, Last annotation update)	
AC	047605; 01-NOV-1996 (TREMBLrel. 01, Last sequence update)		GP55.	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		Bacteriophage A118,	
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)		Viruses; dsDNA viruses, no RNA stage; Tailed Phages; Siphoviridae.	
DE	C (FRAGMENT).		OX NCBI_TaxID=40521;	
GN	Fischerichia coli		[1]	
OS	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		RP SEQUENCE FROM N.A.	
OC	Escherichia		RA Loessner M.J., Inman R.B.; Lauer P.; Calendar R.;	
OC	Escherichia		PubMed=8577256;	
NCBI_TAXID=562;			RA Loessner M.J., Wendlinger G.; Scherer S.;	
RN			RT "Heterogeneous endolysins in Listeria monocytogenes bacteriophages: a new class of enzymes and evidence for conserved holin genes within the siphoviral lysis cassettes".	
RP	SEQUENCE FROM N.A.		RT Mol. Microbiol. 16:1231-1241(1995).	
RX	Medline=91139577; PubMed=1995588;		RA Loessner M.J., Inman R.B.; Lauer P.; Calendar R.;	
RA	Tao T., Bourne J.C., Blumenthal R.M.;		RT "Complete nucleotide sequence, molecular analysis and genome structure of bacteriophage A118 of Listeria monocytogenes: implications for phage evolution.";	
RT	"A family of regulatory genes associated with type II restriction-		RT Mol. Microbiol. 35:324-340 (2000).	
RT	modification systems".		DR EMBL: AT242593; CAB53843.1; -.	
RT	J. Bacteriol. 173:1367-1375(1991).		DR INVERPRO: IPR00021; -.	
DR	NON_TER 1 1		DR PROSITE: PS00228; TUBULIN_B-AUTOREG; 1.	
FT	NON_TER 1 1		SQ SEQUENCE 21 AA; 2485 MW; 7B5D940B75DCF90 CRC64;	
SQ	SEQUENCE 16 AA; 1853 MW; E46774511496607C CRC64;			
Qy	9 LKEFTVSGN 17		Query Match 27.2%; Score 25; DB 9; Length 21;	
Db	3 LLDFFTIGN 11		Best Local Similarity 40.0%; Pred. No. 1.7e+03; Mismatches 3; Indels 0; Gaps 0;	
RESULT 13			Q9UC89 ID 049883 PRELIMINARY; PRT; 25 AA.	
Q9UC89	Q9UC89 PRELIMINARY; PRT; 17 AA.		Q9UC89 AC 049883; DT 01-JUN-1998 (TREMBLrel. 06, Created)	
ID			DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
AC			DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
Q9UC89;			DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
DE	ONCOFETAL-LAMININ BINDING (COLLAGEN ALPHABETA 1(III))		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
OS	Homo sapiens (Human).		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	
OX	NCBI_TAXID:9606;		DE ALPHA_1(III) CHAIN, OF-LB-COLLAGEN	

GN LOXC HOMOLOGUE.
OS Lycopersicon hirsutum.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=62830;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CV CF4;
RX MEDLINE#98074802; PubMed#9413991;
RA Parniske M., Hammond-Kosack K.E., Colstain C., Thomas C.M.,
RA Jones D.A., Harrison K., Wulff B.B., Jones J.D.;
RT "Novel disease resistance specificities result from sequence exchange
RT between tandemly repeated genes at the Cf-4/9 locus of tomato.";
RL Cell 91:821-832(1997),
DR EMBL; AJ002235; CAA05271.1;
DR HSSP; P08170; YGEE.
FT NON_TER 1 1
SEQUENCE 25 AA; 2710 MW; 72CDC71677C3792F CRC64;

Query Match 27.2%; Score 25; DB 10; Length 25;
Best Local Similarity 46.2%; Pred. No. 2.1e-03;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 4 VPGVLLKEFVSG 16
:| ||| |:
Db 1 MPYELLKPFSEPG 13

Search completed: May 8, 2001, 15:16:06
Job time: 532 sec

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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:05:10 ; Search time 62.11 Seconds
(without alignments)
3.093 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCF1 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210837 residues

Total number of hits satisfying chosen parameters: 110741

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/pctodata/2/iaa/5A_COMB.pep:
2: /cgn2_6/pctodata/2/iaa/5B_COMB.pep:
3: /cgn2_6/pctodata/2/iaa/6A_COMB.pep:
4: /cgn2_6/pctodata/2/iaa/6B_COMB.pep:
5: /cgn2_6/pctodata/2/iaa/PC7US_COMB.pep:
6: /cgn2_6/pctodata/2/iaa/backfile1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	11	4	US-09-183-931-42
2	47	82.5	9	4	US-09-183-931-43
3	35.5	62.3	20	2	US-08-915-84
4	33	57.9	9	4	US-09-183-931-44
5	31	54.4	14	2	US-08-764-640-35
6	31	54.4	14	2	US-08-764-640-36
7	31	54.4	14	3	US-08-973-225-35
8	31	54.4	14	3	US-08-973-225-36
9	31	54.4	14	4	US-09-244-298A-35
10	31	54.4	14	4	US-09-244-298A-36
11	28	49.1	16	5	PCT-US91-02942-14
12	27	48.2	24	2	US-08-470-419-2
13	27	48.2	24	2	US-08-761-828-2
14	27	48.2	24	2	US-08-290-105-2
15	27	48.2	24	3	US-08-776-949-2
16	27	48.2	24	3	US-08-482-810-2
17	27	47.4	19	5	PCT-US93-08435-61
18	27	47.4	20	2	US-08-483-636-6
19	27	47.4	20	2	US-08-83-632-6
20	27	47.4	20	5	PCT-US94-07659-10
21	26	45.6	6	3	US-08-182-528-186
22	26	45.6	6	3	US-08-182-528-186
23	26	45.6	11	1	US-08-451-947-45
24	26	45.6	11	2	US-08-828-845
25	26	45.6	11	3	US-08-928-694-45
26	26	45.6	11	4	US-09-224-785-7
27	26	45.6	11	5	PCT-US91-06950-45

28	26	45.6	12	1	US-08-451-947-24
29	26	45.6	12	2	US-08-424-826A-24
30	26	45.6	12	3	US-08-928-694-24
31	26	45.6	12	5	PCT-US91-06930-24
32	26	45.6	14	1	US-08-311-611A-81
33	26	45.6	14	1	US-08-372-783-81
34	26	45.6	14	1	US-08-306-473A-81
35	26	45.6	14	1	US-08-209-762-81
36	26	45.6	14	1	US-08-473-344-81
37	26	45.6	14	2	US-08-621-803-79
38	26	45.6	14	2	US-08-845-445A-81
39	26	45.6	14	2	US-08-621-255A-25
40	26	45.6	14	3	US-09-119-263-81
41	26	45.6	14	4	US-08-657-162-81
42	26	45.6	14	4	US-09-224-480-81
43	26	45.6	14	5	PCT-US94-02445-81
44	26	45.6	14	5	PCT-US95-00498-81
45	26	45.6	14	5	PCT-US95-00498-81

ALIGNMENTS

RESULT 1
US-09-183-931-42

; Sequence 42, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brassieur, Francis
; APPLICANT: Bonn-Palleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527-1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US/09/0183C
; EARLIER FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 44
SEQ ID NO 42
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-09-183-931-42

Query Match 100 0%; Score 57; DB 4; Length 11;
Best Local Similarity 100 0%; Pred. No. 0.00087;
Matches 10; conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCF1 10
Db 2 LLMWITQCF1 11
RESULT 2
US-09-183-931-43
; Sequence 43, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brassieur, Francis
; APPLICANT: Bonn-Palleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527-1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US/09/0183C
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44

SEQ ID NO 43
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 OTHER INFORMATION:
 US-09-183-931-43

RESULT 4
 US-09-183-931-44
 Sequence 44, Application US/09183931.C
 Patent No. 6210886

GENERAL INFORMATION:
 APPLICANT: Van Baren, Nicolas
 APPLICANT: Bresser, Francis
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
 TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
 FILE REFERENCE: LUD 5527.1-JEL/ES
 CURRENT APPLICATION NUMBER: US/09-183,931.C
 CURRENT FILING DATE: 2000-02-28
 EARLIER APPLICATION NUMBER: US 09/018,422
 EARLIER FILING DATE: 1998 - 02 - 04
 NUMBER OF SEQ ID NOS: 44
 SEQ ID NO 44
 LENGTH: 9

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
 Db 2 LLMWITQC 9

RESULT 3
 US-08-934-915-84
 Sequence 84, Application US/08934915
 Patent No. 5932412

GENERAL INFORMATION:
 APPLICANT: DILLNER, JOAKIM
 APPLICANT: DILLNER, LENA
 APPLICANT: CHENG, HWEE-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 TITLE OF INVENTION: PAPILLOANVIRUS 1, 5, 6, 8,
 TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
 TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MASON & ASSOCIATES, P.A.
 STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 CITY: CLEARWATER
 STATE: FLORIDA
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 3.0
 SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,915
 FILING DATE: 22-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/949,836
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: LOUISE A. FOUTCH
 REGISTRATION NUMBER: 37,133
 REFERENCE/DOCKET NUMBER: 1946.6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 813-538-3800
 TELEFAX: 813-538-3820
 TELEX:
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match 82.3%; Score 35.5; DB 2; Length 20;
 Best Local Similarity 46.7%; Pred. No. 5.1;
 Matches 7; Conservative 3; Mismatches 0; Indels 5; Gaps 1;

RESULT 5
 US-08-764-640-35
 Sequence 35, Application US/08764640
 Patent No. 5869451
 Patent No. 5869451 5837683

GENERAL INFORMATION:
 APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Cwirka, Steven E.
 APPLICANT: Gates, Christian
 APPLICANT: Schatz, Peter J.
 APPLICANT: Balasubramanian, Palaniappan
 APPLICANT: Wagstrom, Christopher R.
 APPLICANT: Hendren, Richard W.
 APPLICANT: Deprince, Randolph B.
 APPLICANT: Podduturi, Surekha
 APPLICANT: Yin, Qun
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,640
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514

Qy 1 LLMWIT----QCFL 10
 Db 2 LLMWITQC 9

ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-764-640-35

RESULT 6
 US-08-764-640-36
 Sequence 36, Application US/08764640
 Patent No. 5869451 5837683
 GENERAL INFORMATION:

APPLICANT:	Dover, William J.
APPLICANT:	Barrett, Ronald W.
APPLICANT:	Cwirla, Steven E.
APPLICANT:	Gates, Christian
APPLICANT:	Schatz, Peter J.
APPLICANT:	Balasubramanian, Palaniappan
APPLICANT:	Wagstrom, Christopher R.
APPLICANT:	Hendren, Richard W.
APPLICANT:	Deprince, Randolph B.
APPLICANT:	Podduturi, Surekha
APPLICANT:	Yiu, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 NUMBER OF SEQUENCES: 244
 CURRENT APPLICATION DATA:
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 APPLICATION NUMBER: US/08/764-640
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 US-08-764-640-36

Query Match 54.4%; Score 31; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1 LLMWITQC 8
Db	1 :
Db	7 LLEWLTLIC 14

RESULT 7
 US-08-973-225-35
 Sequence 35, Application US/08973225A
 Patent No. 6083913
 GENERAL INFORMATION:
 APPLICANT: Dover, William J.
 Barrett, Ronald W.
 Cwirla, Steven E.
 Duffin, David J.
 Gates, Christian
 Haselden, Sherril S.
 Mattheakis, Larry C.
 Schatz, Peter J.
 Wagstrom, Christopher R.
 Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 NUMBER OF SEQUENCES: 232
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973-225A
 FILING DATE: 04-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3065USW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Query Match 54.4%; Score 31; DB 3; Length 14;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1 LLMWITQC 8
Db	1 :
Db	7 LLEWLTLIC 14

RESULT 8

APPLICANT: Yin, Qun
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 TITLE OF INVENTION: RECEPTOR
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09/244,298A
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-244-298A-35

Query Match 54.4%; Score 31; DB 3; Length 14;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

RESULT 10
 US-09-244-298A-36

Sequence 36, Application US-09244298A
 Patent No. 6121238

GENERAL INFORMATION:
 APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Cwirla, Steven E.
 APPLICANT: Gates, Christian
 APPLICANT: Schatz, Peter J.
 APPLICANT: Balasubramanian, Palaniappan
 APPLICANT: Wagstrom, Christopher R.
 APPLICANT: Hendren, Richard W.
 APPLICANT: Deprince, Randolph B.
 APPLICANT: Podduturi, Surekha
 APPLICANT: Yin, Qun
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 TITLE OF INVENTION: RECEPTOR
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09/244,298A
 FILING DATE: 04-DEC-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: <unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Query Match 54.4%; Score 31; DB 3; Length 14;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

RESULT 9
 US-09-244-298A-35

Sequence 35, Application US-09244298A
 Patent No. 6121238

GENERAL INFORMATION:
 APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Cwirla, Steven E.
 APPLICANT: Gates, Christian
 APPLICANT: Schatz, Peter J.
 APPLICANT: Balasubramanian, Palaniappan
 APPLICANT: Wagstrom, Christopher R.
 APPLICANT: Hendren, Richard W.
 APPLICANT: Deprince, Randolph B.
 APPLICANT: Podduturi, Surekha
 APPLICANT: Yin, Qun
 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 TITLE OF INVENTION: RECEPTOR
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09/244,298A
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PCT3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-244-298A-36

Query Match 54.4%; Score 31; DB 4; Length 14;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LMWLTQC 8
 Db 7 LLEWLFLC 14

RESULT 11
 PCT-US91-02942-14
 Sequence 14 Application PC/TUS9102942
 GENERAL INFORMATION:
 APPLICANT: ROTHLEIN, ROBERT
 ATTORNEY: ADAIR, JOHN R.
 APPLICANT: ATHWAL, DILJEET S
 TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
 NUMBER OF SEQUENCES: 102
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 ADDRESS: Sterne, Kessler, Goldstein & Fox
 STREET: 1225 Connecticut Ave. NW Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/02942
 FILING DATE: 1991-04-29
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9009549.8
 FILING DATE: 27-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: FOX, SAM L.
 REGISTRATION NUMBER: 30,353
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 466-0800
 TELEFAX: (202) 833-8716
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 49.1%; Score 28; DB 5; Length 16;
 Best Local Similarity 66.7%; Pred. No. 69;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMWLT 6
 Db 11 LMWLT 16

RESULT 12
 US-08-470-419-2
 Sequence 2, Application US/08470419
 Patent No. 5866320
 GENERAL INFORMATION:
 APPLICANT: ROVINSKI, Benjamin
 APPLICANT: CAO, Shi-Xian
 APPLICANT: YAO, Fei-Long
 APPLICANT: PERSSON, Roy
 APPLICANT: KLEIN, Michel H
 TITLE OF INVENTION: ANTIGENICALLY-MARKED NON-INFECTIOUS
 TITLE OF INVENTION: RETROVIRUS-LIKE PARTICLES
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: Suite 701, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470-419
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: 1038-385 MIS:jb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-470-419-2

Query Match 48.2%; Score 27.5; DB 2; Length 24;
 Best Local Similarity 41.7%; Pred. No. 1.2e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

Qy 2 LMWLT--QCFL 10
 Db 2 ILMISFAISCFL 13

RESULT 13
 US-08-761-828-2
 Sequence 2, Application US/08761828
 Patent No. 5879925

GENERAL INFORMATION:
 APPLICANT: ROVINSKI, Benjamin
 APPLICANT: CAO, Shi-Xian
 APPLICANT: YAO, Fei-Long
 APPLICANT: PERSSON, Roy
 APPLICANT: KLEIN, Michel H
 TITLE OF INVENTION: ANTIGENICALLY-MARKED NON-INFECTIOUS RETROVIRUS-LIKE PARTICLES
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: 6TH Floor, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/290,105
 FILING DATE: August 15, 1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: STEWART, Michael I
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-385 MIS:jb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INQUIRIES FOR SEQ ID NO: 2;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-290-105-2

Query Match Score 48.2%; Score 27.5%; DB 2; Length 24;
 Best Local Similarity 41.7%; Pred. No. 1.2e+02; Indels 3; Gaps 1;

Match 5; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

RESULT 15
 US-08-776-949-2
 Sequence 2, Application US/08776949
 Patent No. 6025125

GENERAL INFORMATION:
 NAME: STEWART, Michael I
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-655 MIS:jb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INQUIRIES FOR SEQ ID NO: 2;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-776-949-2

Query Match Score 48.2%; Score 27.5%; DB 2; Length 24;
 Best Local Similarity 41.7%; Pred. No. 1.2e+02; Indels 3; Gaps 1;

Match 5; Conservative 3; Mismatches 1; Indels 3; Gaps 1;

Qy 2 LMWIT--QCFL 10
 : : : :
 Db 2 ILWISFAISCFL 13

RESULT 14
 US-08-290-105-2
 Sequence 2, Application US/08290105
 Patent No. 5955342

GENERAL INFORMATION:
 APPLICANT: ROVINSKI, Benjamin
 APPLICANT: CAO, Shi-Xian
 APPLICANT: YAO, Fei-Long
 APPLICANT: PERSSON, Roy
 APPLICANT: KLEIN, Michel H
 TITLE OF INVENTION: ANTIGENICALLY-MARKED NON-INFECTIOUS RETROVIRUS-LIKE PARTICLES
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: Suite 701, 330 University Avenue
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 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,949
 FILING DATE: 02-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: STEWART, Michael I
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-673 MIS:jb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
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 INQUIRIES FOR SEQ ID NO: 2;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 amino acids
 TYPE: amino acid

Tue May 8 15:56:42 2001

us-09-165-546a-7.raii

Page 7

; STRANDEDNESS: single
; TOPOLOGY: linear
us-08-776-949-2

Query Match 48.2%; Score 27.5; DB 3; Length 24;
Best Local Similarity 41.7%; Pred. No. 1.2e+00;
Matches 5; Conservative 3; Mismatches 1; Indels 3; Gaps 1;
Qy 2 LMWIT--QCFL 10
 ::|:|:
Db 2 ILWISFAISCEL 13

Search completed: May 8, 2001, 15:05:10
Job time: 106 sec

., Gencore version 4.5
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OM protein - protein search, using sw model
Run on: May 8, 2001, 15:08:18 ; Search time 68.24 Seconds
(without alignments)
10.071 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 6872935 residues

Total number of hits satisfying chosen parameters: 4929

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_67:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	43.9	24	F24406	unspecific monooxygenase (EC 1.14.14.1), 53K, 3-methylcholanthrene-inducible, hepatic
2	24	42.1	23	S31210	N: Alternative names: cytochrome P450
3	23	40.4	19	S60633	C: Species: Cavia porcellus (guinea pig)
4	23	40.4	23	PH1361	C: Date: 21-May-1998 #sequence_revision 21-May-1998 #text_change 05-Mar-1999
5	23	40.4	25	B36934	C: Accession: F24406
6	22	38.6	10	P70289	R: Cheng, K.C.; Park, S.S.; Krutzsch, H.C.; Grantham, P.H.; Gelboin, H.V.; Friedman, F
7	22	38.6	12	JS0424	Biochemistry, 25, 2397-2402, 1986
8	22	38.6	12	JS0424	A: Title: Amino-terminal sequence and structure of monoclonal antibody immunopurified
9	22	38.6	18	S158273	A: Reference number: A24406; MUID:86243357
10	22	38.6	22	S19914	A: Molecule type: Protein
11	21	36.8	20	S07817	A: Residues: 1-24 <GUE>
12	21	36.8	23	B33761	C: Superfamily: human cytochrome P450 homology
13	21	36.8	24	E53613	C: Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembr
14	21	36.8	24	A36912	ALIGNMENTS
15	20	35.1	7	S09652	Query Match 1 LLMWITQCFL 9
16	20	35.1	7	PX0008	Best Local Similarity 43.9%; Score 25; DB 2; Length 24;
17	20	35.1	9	S07241	Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
18	20	35.1	10	T17075	Query Match 1 LLMWITQCFL 9
19	20	35.1	13	PQ0445	Best Local Similarity 33.3%; Score 25; DB 2; Length 24;
20	20	35.1	17	S05917	Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
21	20	35.1	20	S38763	Query Match 1 LLMWITQCFL 9
22	20	35.1	21	PQ0119	Best Local Similarity 33.3%; Score 25; DB 2; Length 24;
23	20	35.1	22	A35418	Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
24	20	35.1	22	S06487	Query Match 1 LLMWITQCFL 9
25	20	35.1	22	S42567	Best Local Similarity 33.3%; Score 25; DB 2; Length 24;
26	20	35.1	24	S01808	Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
27	19	33.3	8	S19288	Query Match 1 LLMWITQCFL 9
28	19	33.3	13	B19434	Best Local Similarity 33.3%; Score 25; DB 2; Length 24;
29	19	33.3	17	B232219	Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 11 LLAVTSC 18
 RESULT 3
 S66533 H+ transporting ATP synthase (EC 3.6.1.34) protein 8 - brine shrimp mitochondrial (strain H+; species: mitochondrial Artemia sp. (brine shrimp))
 A; Variety: strain La Mata
 C; Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-Dec-1999
 C; Accession: S66533
 R; Perez, M.L.; Valverde, J.R.; Betuecas, B.; Amat, F.; Marco, R.; Garesse, R.
 J. Mol. Evol. 38, 156-168, 1994
 A; Title: Specification in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic
 A; Reference number: S6624; MUID_94223692
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecular type: DNA
 A; Residues: 1-19 <PER>
 A; Cross-references: EMBL:X67263; PID:911210; PIDN:CAA47685.1; PID:911211
 A; Experimental source: strain La Mata
 C; Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; oxido-reductase
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 C; Genetics:
 A; Gene: ATP8
 A; Genome: mitochondrial
 A; Genetic code: SCC4
 A; Superfamily: H+-transporting ATP synthase protein 8
 C; Superfamily: ATP synthase; hydrolase; membrane-associated complex; mitochondrion; oxido-reductase
 A; Note: the source is designated as Artemia parthenogenetica
 C; Species:
 A; Accession: PT0289
 A; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A; Title: preferential utilization of specific immunoglobulin heavy chain diversity an
 A; Reference number: PT0222; MUID:91108337
 A; Accession: PT0289
 A; Molecular type: DNA
 A; Residues: 1-10 <YAM>
 A; Experimental source: B lymphocyte
 C; Keywords: heterotetramer; immunoglobulin
 Query Match 40.4%; Score 23; DB 2; Length 19;
 Best Local Similarity 62.5%; Pred. No. 6.e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 LMMWITQCF 9
 Db 7 LPNTIFF 14
 RESULT 4
 PH1361 Ig heavy chain DJ region (clone C178-122B) - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C; Accession: PH1361
 R; Wasserman, R.; Gallit, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A; Title: Predominance of fetal type DJH joining in young children with B precursor lymphocytes
 A; Reference number: PH1302; MUID:93094761
 A; Accession: PH1361
 A; Molecular type: DNA
 A; Residues: 1-23 <WAS>
 C; Superfamily: immunoglobulin V region; immunoglobulin homology
 C; Keywords: heterotetramer; immunoglobulin
 Query Match 40.4%; Score 23; DB 2; Length 23;
 Best Local Similarity 33.3%; Pred. No. 7.6e+02;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 LMMWITQCF 9
 Db 1 VLLWFGEFL 9
 RESULT 5
 B36334 orf3' of mada - Thiobacillus versutus (fragment)
 C; Species: Thiobacillus versutus
 C; Accession: B36934
 C; Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 03-Mar-1995
 R; Huittema, F.; van Beumen, J.; van Driessche, G.; Duine, J.A.; Canters, G.W.
 J. Baert et al., 175, 6254-6259, 1993
 RESULT 8
 158273

A; Title: Cloning and sequencing of the gene coding for the large subunit of methylami
 A; Reference number: A36934; MUID:94012487
 A; Accession: B36934
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-25 <HUI>
 A; Experimental source: ATCC 25364T
 A; Note: sequence extracted from NCBI backbone (NCBIN:138060, NCBIP:138062)

Query Match 40.4%; Score 23; DB 2; Length 25;
 Best Local Similarity 40.0%; Pred. No. 8.2e+02;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LMMWITQCFL 10
 Db 9 LIHWALRSFL 18

RESULT 6
 PT0289
 19 heavy chain CRD3 region (clone 4-109) - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C; Accession: PT0289
 R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A; Title: preferential utilization of specific immunoglobulin heavy chain diversity an
 A; Reference number: PT0222; MUID:91108337
 A; Accession: PT0289
 A; Molecular type: DNA
 A; Residues: 1-10 <YAM>
 A; Experimental source: B lymphocyte
 C; Keywords: heterotetramer; immunoglobulin
 Query Match 38.6%; Score 22; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMMWIT 6
 Db 1 LLNWIS 6

Query Match 38.6%; Score 22; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMMWIT 6
 Db 1 LLNWIS 6

RESULT 7
 JS0424 urotensin II-B peptide - white sucker
 C; Species: Catostomus commersoni (white sucker)
 C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
 C; Accession: JS0424
 Peptides 4, 367-373, 1983
 A; Title: Isolation and amino acid sequence of two urotensin II peptides from Catostom
 A; Accession: JS0424
 A; Molecular type: protein
 A; Residues: 1-12 <MCM>
 C; Comment: This peptide has smooth muscle-stimulating activity.
 F; 6-11/Disulfide bonds: #status experimental

Query Match 38.6%; Score 22; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 6.4e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TQCF 9
 Db 4 TECF 7

thyroglobulin - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 15273
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 R;Musti, A.M.; Ursini, V.M.; Avvedimento, E.V.; Zimarino, V.; Di Lauro, R.
 Nucleic Acids Res. 15, 8149-8166, 1987
 A;Title: A cell type specific factor recognizes the rat thyroglobulin promoter.
 A;Reference number: 158273; MUID:88040446
 A;Accession: 158273
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-12 <REF>
 A;Cross-references: EMBL:X06162; NID:957368; PIDN:CAA29519.1; PID:957369

Query Match 9
 Best Local Similarity 33.3%; Score 38.6%; Pred. No. 6.4e+02; Length 12;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
 Db 4 LVLWVS 9

RESULT 9
 S19914 choline O-acetyltransferase (EC 2.3.1.6) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Accession: S19914
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-May-2000
 R;Toussaint, J.-L.; Bausero, P.; Stricker, C.; Geoffroy, V.; Simoni, P.; Kempf, J.; Schmit submitted to the EMBL Data Library, March 1992
 A;Description: Human choline acetyltransferase gene: analysis of transcription control r
 A;Reference number: S19914
 A;Accession: S19914
 A;Molecule type: DNA
 A;Residues: 1-18 <TOU>
 A;Cross-references: EMBL:X65023
 C;Keywords: acyltransferase; coenzyme A

Query Match 9
 Best Local Similarity 60.0%; Score 38.6%; Pred. No. 9.2e+02; Length 18;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 MWITQ 7
 Db 7 LWVTP 11

RESULT 10
 S07817 spike glycoprotein precursor - rabies virus (fragment)
 N;Alternate names: transmembrane glycoprotein G
 C;Species: rabies virus
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Sep-1999
 C;Accession: S07817
 R;Poch, O.; Tordo, N.; Keith, G.
 Biochimie 70, 1019-1029, 1988
 A;Title: Sequence of the 3'86 3' nucleotides of the genome of the AVO1 strain rabies virus
 A;Accession: S07813; MUID:89150295
 A;Residues: 1-22 <POC>
 A;Cross-references: EMBL:X13357; NID:961809; PIDN:CAA31737.1; PID:961814
 C;Genetics:
 A;Gene: G
 C;Superfamily: rabies virus spike glycoprotein
 C;Keywords: glycoprotein; transmembrane protein

Query Match 10
 Best Local Similarity 44.4%; Score 38.6%; Pred. No. 1.1e+03; Length 22;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9
 Db 10 LLGQFSLCF 18

RESULT 11
 B33761 actin - Acanthamoeba castellanii (fragment)
 C;Species: Acanthamoeba castellanii
 C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 12-Apr-1995
 R;Vandekerckhove, J.S.; Kaiser, D.A.; Pollard, T.D.
 J. Cell Biol. 109, 619-626, 1989
 A;Title: Acanthamoeba actin and profilin can be cross-linked between glutamic acid 36
 A;Reference number: A33761; MUID:893340644
 A;Accession: B33761
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <PAN>
 C;Superfamily: actin

Query Match 11
 Best Local Similarity 75.0%; Score 36.8%; Pred. No. 1.5e+03; Length 20;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITQ 7
 Db 1 WITK 4

RESULT 12
 S65141 nucleotide triphosphatase - garden pea (fragments)
 C;Species: Pisum sativum (garden pea)
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
 C;Accession: S65141
 R;Isieh, H.L.; Tong, C.G.; Thomas, C.; Roux, S.J.
 Plant Mol. Biol. 30, 135-147, 1996
 A;Title: Light-modulated abundance of an mRNA encoding a calmodulin-regulated chroma
 A;Reference number: S65141; MUID:96197404
 A;Accession: S65141
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15;16-23 <HSI>

Query Match 13
 Best Local Similarity 50.0%; Score 36.8%; Pred. No. 1.7e+03; Length 23;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MWIT 6
 Db 17 LWVT 20

RESULT 13
 E53613 plectoxin XIII - spider (Plectreurus tristis)
 C;Species: Plectreurus tristis
 C;Accession: E53613
 R;Quistad, G.B.; Skinner, W.S.
 J. Biol. Chem. 269, 11088-11101, 1994
 A;Title: Isolation and sequencing of insecticidal peptides from the primitive hunting
 A;Reference number: A53613; MUID:94209277
 A;Accession: E53613
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-24 <QUI>
 C;Superfamily: curtaoxin

Query Match 36.8%; Score 21; DB 2; Length 24;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 WITOC 8
 |:
 Db 7 WBYTC 11

RESULT 14

A36912 hypothetical protein 1 baig-region [imported] - Eubacterium sp. (fragment)
 C;Species: Eubacterium sp.
 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
 C;Accession: A36912
 R;Franklund, C.V.; Baron, S.F.; Hylemon, P.B.
 J;Bacteriol. 175, 3002-3012, 1993
 A;Title: Characterization of the baiH gene encoding a bile acid-inducible NADH:flavin ox
 A;Reference number: A36912; MUID:93259945
 A;Accession: A36912
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-124 <PRA>
 A;Experimental source: VPI 12708
 A;Note: sequence extracted from NCBI backbone (NCBIN:131883, NCBIPI:131906)

Query Match 36.8%; Score 21; DB 2; Length 24;
 Best Local Similarity 42.9%; Pred. No. 1.8e+03;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LIMWITQ 7
 |:::|||
 Db 7 LILFLTQ 13

RESULT 15

S09652 hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)
 C;Species: Enterobacter cloacae
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
 C;Accession: S09652
 R;Vliegenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.
 Antimicrob. Agents Chemother. 33, 1153-1159, 1989
 A;Title: Nucleotide sequence of the aacc2 gene, a gentamicin resistance determinant inv
 A;Reference number: S09651; MUID:90024972
 A;Accession: S09652
 A;Molecule type: DNA
 A;Residues: 1-7 <VLI>
 A;Cross-references: EMBL:X51534; PID:CAA35914.1; PID:g581034

Query Match 35.1%; Score 20; DB 2; Length 7;
 Best Local Similarity 40.0%; Pred. No. 2e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LIMWI 5
 ::|||
 Db 1 MIWI 5

Scoring table:	BLOSUM62	34	16	28.1	20	1	LYC_FELCA
Gapop:	10.0	35	16	28.1	24	1	LCA_FELCA
Gapext:	0.5	36	16	28.1	24	1	PQQ_ACICA
Searched:	93435 seqs., 34255486 residues	37	15	26.3	5	1	UF01_BOVIN
Total number of hits satisfying chosen parameters:	1423	38	15	26.3	9	1	P29177_bos_taurus
Minimum DB seq length:	0	39	15	26.3	9	1	P42996_scyllorhinus
Maximum DB seq length:	25	40	15	26.3	9	1	P42999_squalus_acanthias
Post-processing:	Minimum Match 0%	41	15	26.3	10	1	P80474_capnocytophaga
	Maximum Match 100%	42	15	26.3	10	1	P81084_pinus_pins
Database :	Swissprot_39; *	43	15	26.3	12	1	P04558_catostomus
Sequence:	1 LIMWITQCFL 10	44	15	26.3	12	1	P01147_gilllichthys
		45	15	26.3	13	1	Q05311_salmonella
ALIGNMENTS							
Scoring table:	BLOSUM62	RESULT 1					
Gapop:	10.0 , Gapext 0.5	ID UR2B_CATCO	STANDARD;		PRT;	12 AA.	
Searched:	93435 seqs., 34255486 residues	ID UR2B_CATCO	STANDARD;		PRT;	12 AA.	
Total number of hits satisfying chosen parameters:	1423	AC P04559;					
Minimum DB seq length:	0	DT 13-AUG-1987 (Rel. 05, Created)					
Maximum DB seq length:	25	DT 13-AUG-1987 (Rel. 05, Last sequence update)					
Post-processing:	Minimum Match 0%	DT 01-OCT-2000 (Rel. 40, Last annotation update)					
	Maximum Match 100%	DE UROTENSIN_IIB (U-IIB) (UTIB).					
Database :	Swissprot_39; *	OS Catostomus commersoni (White sucker).					
Sequence:	1 LIMWITQCFL 10	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Actinopterygii; Neopterigii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Catostomidae; Catostomus.					
		NCBI_TaxID=7971;					
		OX [1]					
		RN [1]					
		RP RP					
		SEQUENCE					
		MEDLINE=64041959; PubMed=6138758;					
		RA McMaster D., Lederis K.;					
		"Isolation and amino acid sequence of two urotensin II peptides from Catostomus commersoni urophyses.";					
		RT Peptides 4:367-373(1983).					
		RL CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A CORTICOTROPIN-RELEASING FACTOR.					
		CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.					
		PIR; JS0424; JS0424;					
		DR DR					
		InterPro; IPR001483; -					
		DR Pfam; PF02083; Uroteins_in_II; 1.					
		DR PROSITE; PS03984; UROTENSIN_II; 1.					
		KW Hormone.					
		FT FT DISULFID 6 11					
		SQ SEQUENCE 12 AA; 1437 MW; 73961BDDBB879CEBB CRC64;					
		Query Match 38.6%; Score 22; DB 1; Length 12;					
		Best Local Similarity 75.0%; Pred. No. 2.7e+02;					
		Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;					
		YQ 6 TOCF 9					
		Db 4 TECF 7					
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
1	22	38.6	12	1 UR2B_CATCO	P04559 catostomus		
2	22	38.6	12	1 UR2B_CYPKA	P04561 cyprinus ca		
3	22	38.6	22	1 YGLG_RABVA	P15199 rabies virus		
4	21	36.8	12	1 NO4_SOYBN	P55960 glycine max		
5	21	36.8	24	1 PLL3_PLETR	P36987 plectreurus		
6	20	35.1	9	1 LTR_PHYRO	P08946 phyllumedus		
7	20	35.1	19	1 DCAM_ACACA	P34039 acanthamoeb		
8	20	35.1	22	1 MLP_RANTIE	P56924 rana tempor		
9	19	33.3	17	1 CHH3_BORMO	P20729 bombyx mori		
10	19	33.3	20	1 COXA_THUBO	P80972 thunnus obesus		
11	19	33.3	23	1 POOA_KLEPN	P27503 klebsiella		
12	19	33.3	24	1 COXC_THUBOB	P80973 thunnus obesus		
13	19	33.3	24	1 P5AC_CUCSA	P42046 cucumis sat		
14	18	31.6	9	1 DNFI_LOCMI	P16339 locusta mig		
15	18	31.6	11	1 RANC_RANPI	P08951 rana pipiens		
16	18	31.6	12	1 UR2_POLSP	P81022 polyodon sp		
17	18	31.6	13	1 NO40_VICSA	P55961 vicia sativa		
18	18	31.6	17	1 RANR_RANRU	P08952 rana rugosa		
19	18	31.6	20	1 COGL_CHIOP	P34153 chionoecete		
20	18	31.6	24	1 CLPP_HORVU	P48883 bacteriophaga		
21	18	31.6	25	1 Y15_BPT3	P49834 odontella s		
22	18	31.6	25	1 YCX8_ODOSI	P05486 conus geographus		
23	17	29.8	9	1 CONO_CONGE	P42559 manduca sexta		
24	17	29.8	15	1 ALLS_MANSE	P31718 rhodococcus		
25	17	29.8	20	1 CPXX_RHORH	P27436 rattus norvegicus		
26	17	29.8	23	1 TRYL_RATF	P42993 cyprinus carpio		
27	16	28.1	9	1 ISOT_CYPCA	P42998 eisentia foetida		
28	16	28.1	9	1 OXYT_EISFO	P42994 raja clavata		
29	16	28.1	9	1 OXYT_RAJCL	P35490 scyllorhinus		
30	16	28.1	12	1 UR2_SCYCA	P20404 locusta migratoria		
31	16	28.1	16	1 LPK1_LOCM1	P82358 acanthoscorpius		
32	16	28.1	18	1 GONE_ACAGO	P08609 scyllorhinus		
33	16	28.1	18	1 TRN2_SCYCA			

SEQUENCE.
 RA Munekata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
 RL (In) Rich D.H., Gross E. (eds.);
 RL Pierce Chemical Co., Rockford IL. (1981).
 CC :-!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CORTICOTROPIN RELEASING FACTOR.
 CC :-!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
 DR InterPro; IPR01433; -.
 DR Pfam; PF02083; Urotensin_II; 1.
 DR PROSITE; PS00984; UROTENSIN_II; 1.
 KW Hormone.
 FT DISULFID 6 11
 FT VARIANT 2 2 G->S.
 SEQUENCE 12 AA; 1407 MW; 73960A9FF879CBBB CRC64;

Query Match 38.6%; Score 22; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 2.7e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 TOCF 9
 Db 4 TECF 7

RESULT 3
 VGLG_RABVA ID VGLG_RABVA STANDARD; PRT; 22 AA.
 AC P15199;
 DT 01-APR-1990 (Rel. 14; Created)
 DT 01-APR-1990 (Rel. 14; Last sequence update)
 DE SPIKE GLYCOPROTEIN PRECURSOR (FRAGMENT).
 GN G.
 OS Rabies virus (strain Av01).
 OC ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OC NCBI_TaxID=11293;
 RN 11
 RP SEQUENCE FROM N.A. MEDLINE=8910295; PubMed=3147698;
 RA Poch O., Tordo N., Keith G.;
 RT "Sequence of the 3386 3' nucleotides of the genome of the Av01 strain
 in transcription";
 RT Biochimie 70:1019-1029 (1988).
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 or send an email to license@isb-sib.ch).
 CC EMBL; X13357; CAA11737.1; -.
 DR PIR; S07817.
 KW Transmembrane; Envelope protein; Glycoprotein; Signal.

FT SIGNAL 1 19 SPIKE GLYCOPEPTIDE.
 FT CHAIN 20 >22
 FT NON_TER 22 22
 SEQUENCE 22 AA; 2469 MW; BBA59CE12F3EEF85 CRC64;

Query Match 38.6%; Score 22; DB 1; Length 22;
 Best Local Similarity 44.4%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LIMMITQCF 9
 Db 10* LLGFSLGF 18

RESULT 4
 NO40_SOYBN ID NO40_SOYBN STANDARD; PRT; 12 AA.
 AC P55960;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 15-DEC-1998 (Rel. 37; Last annotation update)
 DE EARLY_NODULIN 40.
 OS ENOD40.
 OS Glycine max (soybean).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicots; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_WILLIAMS;
 RX MEDLINE=94035161; PubMed=8220464;
 RA Yang W.C., Katinakis P., Hendriks P., Smolders A., de Vries F.,
 Spee J., van Kammen A., Bisseling T., Franssen H.;
 RT "Characterization of GMENOD40, a gene showing novel patterns of cell-
 specific expression during soybean nodule development.";
 RL Plant J. 3:573-585 (1993).
 CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
 CC GROWTH REGULATOR THAT ALTERS PHOTOPERIODIC RESPONSES (BY
 CC SIMILARITY).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
 CC DEVELOPMENT.
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 CC or send an email to license@isb-sib.ch).
 CC DR X69154; -; NOT_ANNOTATED_CDS.
 CC KW Nodulation; X69154; -; NOT_ANNOTATED_CDS.
 CC SEQUENCE 12 AA; 1391 MW; 3C6958AE78B1A733 CRC64;
 Qy 2 LMWIT 6
 Best Local Similarity 60.0%; Pred. No. 4.1e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 3 LCWLIT 7
 RESULT 5
 PL13_PLETR ID PL13_PLETR STANDARD; PRT; 24 AA.
 AC P36987;
 DT 01-JUN-1994 (Rel. 29; Created)
 DT 01-JUN-1994 (Rel. 29; Last sequence update)
 DT 01-NOV-1997 (Rel. 35; Last annotation update)
 DE PLECTOXIN XIII (PLTXIII) (PLTXIII) (FRAGMENT).
 OS Plectreutys tristis (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicera; Araneae;
 OC Aranomorphe; Haplogyne; Plectreutys; Plectreutidae; Plectreutrys.
 OX NCBI_TaxID=33319;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=94109277; PubMed=8157635;

Qy 1 Isolation and sequencing of insecticidal peptides from the primitive
 RT hunting spider, Plectreutys tristis (Simon).
 RL J. Biol. Chem. 269:11098-11101(1994).

CC	-!- FUNCTION: POTENT TOXIN THAT MAY PARALYZE AND/OR KILL INSECT PESTS SUCH AS H. VIRESCENS (LEPIDOPTERA), S. EXIGUA (BEET ARMYWORM) AND M. SEXTA (TOBACCO HORNTWORM).	RX	MEDLINE=94029912; PubMed=8216217;
CC	-!- PIM: MAY POSSESS FIVE DISULFIDE BONDS.	RA	Hugo E.R., Byers T.J.;
KW		RT	"S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii (Neff); purification and properties.";
FT	NON_TER 24 24 MN; F74A6888E80B0A9A CRC64;	RL	Biochem. J. 295:203-209 (1993).
SQ	SEQUENCE 24 AA; 2745 MN;	CC	-!- FUNCTION: S-ADENOSYLMETHIONINE DECARBOXYLASE IS ESSENTIAL FOR THE BIOSYNTHESIS OF SPERMINE AND SPERMIDINE. THE ALPHA SUBUNIT CONTAINS THE ACTIVE SITE.
Qy	Query Match 6	CC	-!- CATALYTIC ACTIVITY: S-ADENOSYLMETHIONINE = (5'-DEOXY-5'-ADENOSYL)-(3'-AMINOPROPYL)METHYLSULFONIUM SALT + CO(2).
	Best Local Similarity 40.0%; Pred. No. 7.8e+02; Length 24; Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	CC	-!- COFACTOR: REQUIRES A PYRUVOYL GROUP FOR ITS ACTIVITY.
		CC	-!- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE BIOSYNTHESIS FROM PUTRESCINE.
		CC	-!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
		CC	-!- INDUCTION: EXPRESSED ONLY DURING EXPONENTIAL GROWTH.
		CC	-!- INDUCTION: STIMULATED BY PUTRESCINE, INHIBITED BY AROMATIC DIAMINES BERENIL, PENTAMIDE, PROPAIMIDE, HYDROXYSTILBAMIDE, BY ETHIDIUM BROMIDE AND METHYLGLYOXAL.
		CC	-!- SIMILARITY: BELONGS TO THE ADOMETIC FAMILY.
		DR	InterPro; IPR01985; -
		DR	PROSITE; PS01336; ADOMETIC; PARTIAL.
		KW	Spermidine biosynthesis; Lyase; Decarboxylase; Pyruvate, CONVERTED TO A PYRUVOYL GROUP.
		FT	MOD_RES 1
		FT	NON_TER 19 19
		SQ	SEQUENCE 19 AA; 2153 MW; 88B18AD9B6142AEF CRC64;
		Query Match 6	Score 20; DB 1; Length 19;
		Best Local Similarity 30.0%; Pred. No. 9.3e+02; Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	Score 20; DB 1; Length 19;
		Db	1 LLMWITQCFL 10 : : :
		Db	3 MFVRWNTKLIL 12
		RESULT 8	Query Match 6
		MLP_RANTE	Score 20; DB 1; Length 19;
		ID	MLP_RANTE STANDARD; PRT; 22 AA.
		AC	P56924;
		DT	30-MAY-2000 (Rel. 39, Created)
		DR	01-OCT-2000 (Rel. 40, Last sequence update)
		DR	01-OCT-2000 (Rel. 40, Last annotation update)
		DE	MELITTIN-LIKE PEPTIDE (MLP).
		OS	OS Rana temporaria (European common frog).
		OC	OC Eukaryota; Metazoa; Chordata; Anura; Neobatrachia; Bufonoidea; Hyliidae;
		OC	OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
		NCBI_TAXID=8394;	NCBI_TAXID=8407;
		RN	RN [1]
		RP	RP SEQUENCE.
		RA	RA PIR: S07241; S07241;
		RA	RA InterPro; IPR000874; -
		RA	RA Pfam; PF0204; Bombezin; 1.
		RA	RA PROSITE; PS00257; BOMBESIN; 1.
		KW	KW Bombezin family; Amidation.
		FT	FT 1 1 PYRROLIDONE CARBOXYLIC ACID.
		FT	FT MOD_RES 9 9 AMIDATION.
		SQ	SQ SEQUENCE 9 AA; 1090 MW; 4ECCC1E881ADC377 CRC64;
		Query Match 7	Score 20; DB 1; Length 9;
		Best Local Similarity 37.5%; Pred. No. 9.3e+01; Matches 3; Indels 0; Gaps 0;	Score 20; DB 1; Length 9;
		Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Score 20; DB 1; Length 9;
		Db	3 MWITQCFL 10 : : :
		Db	2 LWATGFM 9
		RESULT 7	Query Match 7
		DCAM_ACACA	Score 20; DB 1; Length 22;
		ID	DCAM_ACACA STANDARD; PRT; 19 AA.
		AC	AC P24039; 22 AMIDATION.
		DT	01-FEB-1994 (Rel. 28, Created)
		DT	01-FEB-1994 (Rel. 28, Last sequence update)
		DT	01-FEB-1994 (Rel. 28, Last annotation update)
		DE	DE S-ADENOSYLMETHIONINE DECARBOXYLASE ALPHA SUBUNIT (EC 4.1.1.50)
		DE	(ADOMETDC) (FRAGMENT).
		OS	OS Acanthamoeba castellanii (Amoeba).
		OC	OC Eukaryota; Acanthamoebidae; Acanthamoeba.
		NCBI_TAXID=5755;	NCBI_TAXID=5755;
		RN	RN [1]
		RP	RP SEQUENCE, AND CHARACTERIZATION.
		Qy	1 LLMPITQ 7
		Db	16 IVSMWKQ 22

RESULT 9
 CH3_BOMMO STANDARD; PRT; 17 AA.
 ID CH3_BOMMO
 AC P20729;
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
 CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O +
 CC 4 FERRICYTOCHROME C
 CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON-TER 20 20
 SQ SEQUENCE 20 AA; 2404 MW; 7E82E43B7157355E CRC64;

Query Match 33.3%; Score 19; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85083111; PubMed=6439880;
 RA Rodakis G.C., Lecanidou R., Eickbush T.H.;
 RT "Diversity in a chorion multigene family created by tandem
 duplications and a putative gene-conversion event.";
 RL J. Mol. Evol. 20:265-273(1984).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 SILK MOTH
 CC -!- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 BELONG CLASSES A, CA AND HCA.

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CC DR EMBL: X01068; CAB57790.1; -
 DR PIR; B23219; B23219.
 KW Eggshell; Chorion; Repeat; Multigene family; Signal.
 FT SIGNAL 1 >17
 FT NON-TER 17 17
 SQ SEQUENCE 17 AA; 1913 MW; 5E634508C5355C9C CRC64;

Query Match 33.3%; Score 19; DB 1; Length 17;
 Best Local Similarity 30.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 DB 7 LLQCYQGCLJ 16

RESULT 10
 COXA_THUOB STANDARD; PRT; 20 AA.
 ID COXA_THUOB
 AC P80972;
 CC -1- FUNCTION: 35, Created
 CC 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC CYTOCHROME C OXIDASE POLYPEPTIDE VA-1 (EC 1.9.3.1) (FRAGMENT).
 CC Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Scombridae; Thunnus.
 OC NCBI_TaxID=8241;
 RP SEQUENCE,
 RC TISSUE=Heart, and Liver;
 RX MEDLINE=91454391; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 CC "The" subunit structure of cytochrome-c oxidase from tuna heart and

Query Match 33.3%; Score 19; DB 1; Length 23;
 Best Local Similarity 37.5%; Pred. No. 1.6e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 MMITQCFL 10
 DB 1 MWKKPATI 8

RESULT 12

COXC_THUOB ID COXC_THUOB AC P0977; DT 01-NOV-1997 (Rel. 35, Created) DT 01-NOV-1997 (Rel. 35, Last sequence update)	STANDARD; PRT; 24 AA.	DR Pfam; PF00037; fert; 1. DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1. KW Photosynthesis; Chloroplast; Photosystem I; Iron-sulfur; 4Fe-4S. FT INT-MET 0 0
DE CYTOCHROME C OXIDASE POLYPEPTIDE VA-2 (EC 1.9.3.1) (FRAGMENT). OS Thunnus obesus (Bigeye tuna). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei; Scorpaenidae; Thunnus. NCBI_TaxID=8241; RN [1] RP SEQUENCE.		DR MEDLINE=97454291; PubMed=9310366; RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F., Kadenbach B.; RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver." RL Eur. J. Biochem. 248:99-103 (1997). CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT. CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + CC 4 FERRICYTOCHROME C. CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE. CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY. KW Oxidoreductase; Heme; Mitochondrion; Inner membrane. FT NON_TER 24 24 SEQUENCE 24 AA; 2903 MW; 20998FB91F22E43B CRC64;
Query Match 33.3%; Score 19; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR Query Match 33.3%; Score 19; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR Query Match 33.3%; Score 19; DB 1; Length 24; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 WIT 6 : Db 15 WIT 17	RESULT 14 DNFL_LOCMI STANDARD; PRT; 9 AA. ID DNFL_LOCMI AC P16339; DT 01-AUG-1990 (Rel. 15, Created) DT 01-AUG-1990 (Rel. 37, Last sequence update) DT 15-DEC-1998 (Rel. 37, Last annotation update) DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2). OS Locusta migratoria (Migratory locust). OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera; OC Acridomorpha; Acridoidea; Acriidae; Locusta. NCBI_TaxID=7004; RN [1] RP SEQUENCE.	DR Query Match 33.3%; Score 19; DB 1; Length 24; Best Local Similarity 66.7%; Pred. No. 1.7e+03; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0; SQ 4 WIT 6 : Db 15 WIT 17
RESULT 13 PSAC_CUCSA ID PSAC_CUCSA AC P4046; DT 01-NOV-1995 (Rel. 32, Created) DT 01-NOV-1995 (Rel. 32, Last sequence update)	STANDARD; PRT; 24 AA.	RC TISSUE=Suboesophageal ganglion, and thoracic ganglion; RX MEDLINE=8807077; PubMed=3684410; RA Proux J.-P., Miller C.A., Li J.-P., Carney R.L., Girardie A., DeJaage M., Schooley D.A.; RT "Identification of an arginine vasopressin-like diuretic hormone from Locusta migratoria."; RT Biochem. Biophys. Res. Commun. 149:180-186(1987). CC -!- FUNCTION: DIURETIC HORMONE. CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1. CC -!- SIMILARITY: F2 BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. DR PIR: A23477; A29477. DR InterPro: IPR00981; DR Pfam: PF00220; Hormoned_1. DR PROSITE; PS00264; NEURHYPOPHYS_HORM; 1. KW Hormone; Neuropeptide; Amidation. FT DISULFID 1 6 FT DISULFID 1 6 FT MOD_RES 9 9 SEQUENCE 9 AA; 976 MW; 56EB176EB45IA057 CRC64;
OS Cucumis sativus (Cucumber). OS Chloroplast. Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis. NCBI_TaxID=3659; RN [1] RP SEQUENCE. RX MEDLINE=91355209; PubMed=1883835; RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.; "Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing"; RL Biochim. Biophys. Acta 1059:141-148(1991). CC -!- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE PHOTOSYSTEM I COMPLEX. ESSENTIAL FOR PHOTOCHEMICAL ACTIVITY AND STABLE ASSEMBLY OF PSI. CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS. CC RANC_RAPPI DR Mending; 7834; CUCsa_psac; 1. DR InterPro; IPR001450; -.	Query Match 31.6%; Score 18; DB 1; Length 9; Best Local Similarity 75.0%; Pred. No. 9.3e+04; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Query Match 5 ITQC 8 Best Local Similarity 75.0%; Pred. No. 9.3e+04; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RANATENSIN-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 NCBI_TaxID=8404;
 RN {1}
 RP
 SEQUENCE
 RX MEDLINE=04131098; PubMed=611890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/B/RANATENSIN
 CC FAMILY.
 DR InterPro; IPR000874; -.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Bombesin family; Amidation.
 FT MOD_RES 11 11 AMIDATION,
 SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

 Query Match Score 18; DB 1; Length 11;
 Best Local Similarity 31.68; Pred. No. 1.2e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 WITQCFL 10
 | | | | ;
 Db 5 WATGFM 11

Search completed: May 8, 2001, 15:14:05
 Job time: 526 sec

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4 protein - protein search, using sw model						
on : May 8, 2001, 15:16:04 ; Search time 114.89 seconds (without alignments)						
10.202 Million cell updates/sec						
title: US-09-165-546A-7						
perfect score: 57						
sequence: 1 LIMMITOCFL 10						
scoring table: BLOSUM62						
Gapop 10.0 , Gapext 0.5						
searched: 374700 seqs, 117207915 residues						
total number of hits satisfying chosen parameters:	6627					
minimum DB seq length: 0						
maximum DB seq length: 25						
post-processing: Minimum Match 0.8						
Maximum Match 10.0						
Listing first 45 summaries						
database :						
SPTREMBL_15:*						
1: sp_archaea:*						
2: sp_bacteria:*						
3: sp_fungi:*						
4: sp_human:*						
5: sp_invertebrate:*						
6: sp_mammal:*						
7: sp_minic:*						
8: sp_organelle:*						
9: sp_phage:*						
10: sp_plant:*						
11: sp_rhodent:*						
12: sp_unclassified:*						
13: sp_vertebrate:*						
14: sp_virus:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
8	Query	Match	Length	DB	ID	Description
result	No.	Score				
1	30	52.6	11	4	Q9UB69	Q9ue69 homo sapien
2	27	47.4	20	8	Q36127	Q36127 thryophygus
3	25	43.9	23	4	Q9NZ62	Q9nz62 homo sapien
4	24	42.1	18	4	Q9UJZ3	Q9ujz3 homo sapien
5	24	42.1	21	2	Q9S1C0	Q9s1c0 porphyromon
6	24	42.1	21	14	Q83966	Q83966 influenza a
7	23	40.4	11	14	Q84073	Q84073 influenza a
8	23	40.4	16	6	O62810	O62810 equus cabal
9	23	40.4	17	11	Q9UY6	Q9uy6 ratmus sp.
10	23	40.4	19	8	Q31687	Q31687 artemia par
11	23	40.4	23	4	Q9NZ61	Q9nz61 homo sapien
12	23	40.4	24	4	Q9UE18	Q9ue18 homo sapien
13	22	38.6	11	4	Q9UCR1	Q9ucr1 homo sapien
14	22	38.6	12	11	Q63579	Q63579 ratmus norv
15	22	38.6	17	6	P97758	P97758 mus musculus
16	22	38.6	18	8	Q9ZY75	Q9zy75 cecocelius
17	22	38.6	19	4	O76047	O76047 homo sapien
18	22	38.6	20	11	P97907	P97907 mus musculus
19	22	38.6	22	13	Q9W6D7	Q9w6d7 gallus gallu

"Block deletions in the neuraminidase genes from some influenza A viruses of the N1 subtype."

RT Virology 118:229-234(1982);
RL EMBL: AAA43388.1; -.

DR J02563; NON_TER 1 1

FT 21 21

SEQUENCE 21 AA; 2448 MW; 13C6CFB2007E98EF CRC64;

Query Match 42.1%; Score 24; DB 14; Length 21;

Best Local Similarity 42.9%; Pred. No. 6.6e+02; Mismatches 2; Indels 0; Gaps 0;

RESULT 7 ID Q84073 PRELIMINARY; PRT; 11 AA.

Db 10 WINQYI 16

Query 4 WITQCF 10 ID Q84073 PRELIMINARY; PRT; 11 AA.

Db 10 WINQYI 16

RESULT 7 ID Q84073 PRELIMINARY; PRT; 11 AA.

AC Q84073; DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE INFLUENZA A/FPV/ROSTOCK/34 (H1N1) POLYMERASE 3

(SEG 3), 3' END OF VRNA (INITIATOR REGION FOR PROTEIN CODING)

DB (FRAGMENT).

OS Influenza A virus.

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza virus A and B group.

OX NCBI_TaxID=11320; RN [1]

RP SEQUENCE FROM N.A.; MEDLINE=80034428; PubMed=493121;

RA Robertson J.S.; RT "5, and 3' terminal nucleotide sequences of the RNA genome segments of

RT influenza virus."

RL Nucleic Acids Res. 6:3745-3757(1979).

DR EMBL: J02123; AAA43612.1; -.

FT 11 11

SEQUENCE 11 AA; 1400 MW; CC2007F7A6C412C9 CRC64;

Query Match 40.4%; Score 23; DB 14; Length 11;

Best Local Similarity 50.0%; Pred. No. 5.7e+02; Mismatches 2; Indels 0; Gaps 0;

RESULT 8 ID 062810 PRELIMINARY; PRT; 16 AA.

AC 062810; DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)

DE PREGNANCY-ASSOCIATED GLYCOPROTEIN (FRAGMENT).

PAG.

OS Equus caballus (Horse).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796; RN [1]

RP SEQUENCE FROM N.A.

RA Green J.A., Xie S., Roberts R.M.;

RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

DR EMBL: AF061188; AAC15768.1; FT 16 16

SEQUENCE 16 AA; 1830 MW; 733B85DC7AAC213F CRC64;

Query Match 40.4%; Score 23; DB 6; Length 16;

Best Local Similarity 37.5%; Pred. No. 7.9e+02; Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LMWITQCF 9
Db 9 LVTLSCEF 16

RESULT 9 ID Q9QYX6 PRELIMINARY; PRT; 17 AA.

AC Q9QYX6; DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE OLIGODENDROCTE-SPECIFIC UDP-GALACTOSE:CERAMIDE (FRAGMENT).

OS Rattus sp.

OC Schulte S., Stoffel W.;

RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins";

RT Eur. J. Biochem. 233:947-953(1995).

RL SEQUENCE; MEDLINE=96085162; PubMed=85241863;

RA RAJ, Stoffel W.;

RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins";

RT Eur. J. Biochem. 233:947-953(1995).

SO SEQUENCE 17 AA; 2017 MW; 0F92A645FFD7F828 CRC64;

Query Match 40.4%; Score 23; DB 11; Length 17;

Best Local Similarity 42.9%; Pred. No. 8.3e+02; Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LMWITQ 7
Db 1 LIOWLPQ 7

RESULT 10 ID Q31687 PRELIMINARY; PRT; 19 AA.

AC Q31687; DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE ATPEASE SUBUNIT 8 (FRAGMENT).

GN ATPE8.

OS Artemia parthenogenetica.

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;

OC Artemiidae; Artemia.

OX NCBI_TaxID=6663;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=IA MATA;

RX MEDLINE=9422692; PubMed=8169960;

RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;

RT "Speciation in the Artemia genus: mitochondrial DNA analysis of bisexual and parthenogenetic brine shrimps.";

RT J. Mol. Evol. 38:156-168(1994).

DR EMPL: X67263; CAR47685.1; -

KW Mitochondrion.

FT NON_TER 1

FT 19 AA; 2246 MW; 41922AD313E087E3 CRC64;

SEQUENCE 19 AA;

Query Match	40.4%	Score 23;	DB 8;	Length 19;		Matches 3;	Conservative 1;	Mismatches 3;	Indels 0;	Gaps 0;
Best Local Similarity	62.5%;	Pred. No.	9.2e+02;							
Matches 5;	Conservative 0;	Mismatches 0;								
Qy	2 LMWITOCF 9									
Db	7 LPNTIFF 14									
RESULT 11										
Q9N261	PRELIMINARY;	PRT;	23 AA.							
ID	09N261;									
AC	Q9N261;									
DT	01-OCT-2000	(TREMBLrel.	15,	Created)						
DT	01-OCT-2000	(TREMBLrel.	15,	Last sequence update)						
DT	01-OCT-2000	(TREMBLrel.	15,	Last annotation update)						
DE	ATP7B (FRAGMENT).									
DE	ATP7B (FRAGMENT).									
OS	Homo sapiens (Human).									
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
OX	NCBI_TaxID=9606;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RA	Wu Z.Y., Wang N., Mu Rong S.X.;									
RA	"Another hot point mutation of Wilson disease gene in Chinese exon12."									
RT	Chung-Hua I Hsueh Tsa Chih 79:422-423(1999).									
RL										
RN	[2]									
RP	SEQUENCE FROM N.A.									
RA	Wu Z.Y., Wang N., Mu Rong S.X.;									
RA	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.									
DR	EMBL; AAF34876.1; -.									
FT	NON-TER 1	1								
FT	VARIANT 1	21	D	-> G.						
FT	NON-TER 23	23								
SQ	SEQUENCE 23 AA;	2743 MW;	10DCA8665A40804A	CRC64;						
Query Match	40.4%	Score 23;	DB 4;	Length 23;						
Best Local Similarity	40.0%;	Pred. No.	1.1e+03;	Length 23;						
Matches 4;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0;						
Qy	1 LMWITQPL 10									
Db	14 LWWIVIDEI 23									
RESULT 12										
Q9UE18	PRELIMINARY;	PRT;	24 AA.							
ID	Q9UE18;									
AC	Q9UE18;									
DT	01-MAY-2000	(TREMBLrel.	13,	Created)						
DT	01-MAY-2000	(TREMBLrel.	13,	Last sequence update)						
DT	01-MAY-2000	(TREMBLrel.	13,	Last annotation update)						
GN	LAMIN ALPHA 4 (FRAGMENT).									
GN	LAM4.									
OS	Homo sapiens (Human).									
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.									
OX	NCBI_TaxID=9606;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RA	Richards A.J., Lucarrine C., Pope F.M.;									
RT	"The structural organisation of LAMA 4: the gene encoding laminin alpha 4."									
RL	Eur. J. Biochem. 248:15-23(1997).									
DR	EMBL; Y14240; CAA4636.1; -.									
FT	NON-TER 24	24								
SQ	SEQUENCE 24 AA;	2676 MW;	5358D6159B7A7652	CRC64;						
Query Match	40.4%	Score 23;	DB 4;	Length 24;						
Best Local Similarity	42.9%;	Pred. No.	1.1e+03;	Length 24;						

P97758 PRELIMINARY; PRT; 17 AA.
 ID P97758;
 AC P97758;
 DT 01-MAY-1997 (TREMBLrel. 03; Created)
 DT 01-MAY-1997 (TREMBLrel. 03; Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13; Last annotation update)
 DE DBM28 PROTEIN (FRAGMENT).
 GN H-2D.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RPP
 SEQUENCE FROM N_A.
 RC STRAIN=C57BL/6BY-H-2BM28;
 RA Yun T.J., Melvold R.W., Pease L.R.;
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(0).
 DR EMBL: U83304; AAF41021.1; -;
 DR INTERPRO; IPR001039; -;
 DR PFAM; FF00129; MHC_I; 1.
 FT NON_TER 1
 FT 17 17
 SQ 17 AA; 1956 MW; F3149F377C16F196 CRC64;

Query Match Score 22; DB 11; Length 17;
 Best Local Similarity 38.6%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 LMWITQCF1 10
 DB 5 LQWMYGCDFL 13

Search completed: May 8, 2001, 15:16:04
 Job time: 5:30 sec

XX Novel peptides which bind to MHC class I and MHC class II molecules
PT useful for therapeutic and diagnostic purposes
PT
PS Claim 4; Page 22; 49pp; English.
XX Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC (major
CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal, ovary and testis, but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.

XX Sequence 18 AA;

Query Match 100.0%; Score 88; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.8e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Nismatches 0; Indels 0; Gaps 0;

Qy 1 AADHRQLQISIQQQL 18
||| ||| ||| ||| ||| ||| |||
1 aadhrqlqisiqqql 18

RESULT 2
Y06011 standard; Peptide; 10 AA.
XX

AC Y06011;
XX DT 16-AUG-1999 (first entry)
XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
DE NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
XX leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
XX metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
XX uterine cancer; breast cancer; prostate cancer; ovarian cancer;
XX cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
XX liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
XX vaccine; human leukocyte antigen; HLA.
OS Homo sapiens.
XX PN W09918206-A2.
XX PD 15-APR-1999.
XX PR 21-SEP-1998; 98WO-US19609.
XX PR 08-OCT-1997; 97US-0061428.

OS Homo sapiens.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Rosenberg SA, Wang RF;
XX DR WPI; 1999-277270/23.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rosenberg SA, Wang RF;
XX DR WPI; 1999-277270/23.

XX PA Cancer antigen NY ESO1/CAG-3

XX PS Example 10; Page 42; 88pp; English.
XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PA Cancer antigen NY ESO1/CAG-3
XX PS Example 10; Page 42; 88pp; English.
XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PA Cancer antigen NY ESO1/CAG-3

XX PS Example 10; Page 42; 88pp; English.
XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PA Cancer antigen NY ESO1/CAG-3

XX PS Example 10; Page 42; 88pp; English.
XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human ESO-1/CAG-3
CC ORF1 (see X58599). 30 Epitopes (see Y0598-Y06017) were identified.
CC The present Peptide (ranked 24) corresponds to amino acid residues
CC 143-152 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent
CC tumour antigen capable of eliciting an antigen specific immune
CC response by T cells. Cancer peptides (see Y05967-87) derived from
CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
CC vaccines. A claimed method of preventing or inhibiting cancer
CC involves administering a cancer Peptide, with or without an HLA
CC molecule. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, carcinoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX Sequence 10 AA;
SQ Query 5 RQLQLSISSC 14
Match Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Nismatches 0; Indels 0; Gaps 0;
Gaps 0;

response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX Sequence 10 AA;

Query Match Score 53.4%; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;

Qy 6 QLQLSISSSL 53.4%; Score 47; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.05; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; AA: SQ

Db 1 qqlqllsscl 10

RESULT 4
Y06035 standard; Peptide; 9 AA.
XX DT 16-AUG-1999 (first entry)
AC Y06035;
XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX KW ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.
XX OS Homo sapiens.
XX PN W09918206-A2.
XX PD 15-APR-1999.
XX PF 21-SEP-1998; 98WO-US19609.
XX PR 08-OCT-1997; 97US-0061428.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rosenberg SA, Wang RF;
XX DR; 1999-277270/23.
XX PT Cancer antigen NY ESO1/CAG-3
XX Example 10; Page 43; 88pp; English.
XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y06018-7) were identified. The present peptide (ranked 18) corresponds to amino acid residues 148-156 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma,

CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX Sequence 9 AA;

Query Match Score 49.9%; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e-05; Indels 0; Gaps 0;

Qy 10 STSSCLQQL 49.9%; Score 43; DB 20; Length 9;
ID Y79748 standard; Peptide; 9 AA.
XX AC Y79748;
XX DT 10-MAY-2000 (first entry)
DE NY-ESO-1 derived peptide #4.
XX Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1; HLA binding; human leukocyte antigen; cytolytic T cell; CTL; cytosstatic; melanoma; synovial sarcoma.
XX Homo sapiens.
XX OS Homo sapiens.
XX PN WO200000824-A1.
XX PD 06-JAN-2000.
XX PF 25-JUN-1999; 99WO-US14493.
XX PR 26-JUN-1998; 98US-0105839.
PA (LUDW- LUDWIG INST CANCER RES.
XX PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S; Chen Y, Gure A, Old LJ;
XX DR; 2000-170933/15.
XX PT Determining the possible presence of breast, endometrial, colorectal, lung, bladder or head-neck cancer -
XX PS Example 13; Page 26; 40pp; English.
XX A method has been developed for determining the possible presence of a cancer, which is not melanoma or synovial sarcoma. The method comprises assaying a sample taken from the subject to determine the expression of an SSX gene, and determining the expression as a determination of the possible presence of cancer. Expression of SSX1 gene indicates possible presence of breast, endometrial, colorectal, lung, bladder or head-neck cancer. These cancers are also detected by SSX2 and SSX4 gene expression. CC SSX2 gene expression additionally indicates possible presence of ovarian or stomach cancer. CC SSX4 gene also indicates possible presence of ovarian or stomach cancer. CC CC lymphoma, renal cell cancer, glioma and prostate cancer. Expression of SSX5 gene expression indicates the same cancers as SSX1, except breast cancer. Determining expression of SSX gene can be used to monitor CC progress of melanoma or synovial sarcoma, which is not cancer. The CC SSX-derived peptide complex stimulates proliferation of cytolytic T CC cells. This is useful for treating cancer, especially melanoma. Y78464 CC to Y78468 represent specifically claimed HLA binding peptides for use in CC the method of the invention. Z8852 to Z88465 represent PCR primers used CC in the isolation of SSX genes in the exemplification of the present CC invention. Y78469 to Y78500, and Y79684 to Y79762 represent peptides CC derived from SSX proteins or NY-ESO-1, which are used in the

exemplification of the present invention.

Best Local Similarity 100.0%; Pred. No. 3.2e+05; Gaps 0;

```

Query Match Score 43; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0

2y 10 SISSCQLQI 18
       ||||| |
       1 sisccqlq 9

db

```

RESULT 6 Y06037 Y06037 standard: Bent ide: 9 AA

AC XXX OCT 16-AUG-1999 (first entry)
Y603/;

மாண்பும் கணக்கீர்த்தி மூலம் கணக்கு விதம்

es-1A-3 gene; cancer peptide; antigen; non-Hodgkins lymphoma; Hodgkins lymphoma; lung metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; ovarian cancer; prostate cancer; bladder cancer; kidney cancer; pancreatic cancer; sarcoma; tumor; diagnosis; immunotherapy; t-cell; human leukocyte antigen; HLA.

omo sapiens.

99918206-A2.

-APR-1999.

-SEP-1998; 98OM-US19609.

-OCT-1997: 97US-006

SSH) US DEPT HEALTH & HUMAN SERVICES.

senberg SA, Wang RF;

II; 1999-277270/23.

is peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 (see X58599). 30 Epitopes (see Y06018-7) were identified. The present peptide (ranked 20) corresponds to amino acid residues 5-13 of CAG-1 ORF1 (see Y0965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer Peptides (see Y0596-87) derived from portions of CAG-3 and their variants, are useful as cancer vaccines.

Involves administering a cancer peptide, with or without an HLA ligule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and carcinomas such as breast, ovarian, pancreatic and thyroid cancers.

Query	Match
Sequence	9 AA:
SQ	-
AA:	-
Match	A7 78.
Query	CCCGCG AG.
Match	GGGCGG G.

```

Query Match      44.3%; Score 39; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Sequence 9 AA:

RESULT	8	R29045	standard; peptide; 21 AA.
Y79754	ID Y79754 standard; Peptide; 9 AA.	XX	
XX	XX	AC R29045;	
AC	XX	DT 10-FEB-1993 (first entry)	
XX	XX	DE PLA2 inhibitory peptide.	
DT 10-MAY-2000 (first entry)	XX	XX	
XX	XX	KW Phospholipase; A2; human complement factor C3.	
DE NY-ESO-1 derived peptide #10.	XX	XX	
XX	OS Synthetic.	OS	
KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;	XX	PN WO9206997-A.	
KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;	XX	PD 30-APR-1992.	
KW cytostatic; melanoma; synovial sarcoma.	XX	PF 17-OCT-1991; 91WO-JP01424.	
XX	OS Homo sapiens.	XX	
XX	PN WO200000824-A1.	PR 18-OCT-1990; 90JP-0277842.	
XX	PD 06-JAN-2000.	XX	
XX	PA (TEIJIN LTD.	PA (TEIJIN LTD.	
PF 25-JUN-1999; 99WO-US14493.	XX	XX	
XX	PI Azuma C, Imazumi A, Inoue K, Kudo I, Okada M, Suwa Y;	PI	
PR 26-JUN-1998; 98US-0105839.	XX	XX	
XX	WPI; 1992-299656/36.	DR	
PA (LUDWIG) LUDWIG INST CANCER RES.	XX	XX	
XX	Peptide with phospholipase A2 inhibitory activity - originating	PT	
PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;	XX	PT in inflamed parts	
PI Chen Y, Gure A, Old LJ;	XX	Claim 1; Page 8; 15pp; Japanese.	
XX	PS DR; 2000-170933/15.	XX	
XX	Determining the possible presence of breast, endometrial, colorectal,	CC	
PR PR taken from the subject to determine the expression of	CC	CC the peptide has phospholipase A2 inhibitory activity and originates	
lung, bladder or head-neck cancer -	CC	CC in inflamed tissues. Substitutions, additions or deletions may be	
XX made to this sequence resulting in the same activity. This sequence	CC	CC made to this sequence resulting in the same activity. This sequence	
PS Example 13; Page 26; 40pp; English.	CC	CC is identical to a region found between amino acid residue 612 and	
XX	CC PA; 2000-170933/15.	CC the C-terminal of the C3-alpha chain of human complement factor C3.	
CC A method has been developed for determining the possible presence of a	CC	CC The peptide has an IC50 = 500 nM in inhibiting rat and human derived	
CC cancer, which is not melanoma or synovial sarcoma. The method comprises	CC	CC phospholipase A2.	
CC assaying a sample taken from the subject to determine the expression of	CC	CC	
CC an SSX gene, and determining the expression as a determination of the	CC	CC	
CC possible presence of cancer. Expression of SSX1 gene indicates possible	CC	CC	
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck	CC	CC	
CC cancer. These cancers are also detected by SSX2 and SSX4 gene expression.	CC	CC	
CC SSX2 gene expression additionally indicates possible presence of	CC	CC	
CC CC lymphoma, renal cell cancer, glioma and prostate cancer. Expression of	CC	CC	
CC SSX4 gene also indicates possible presence of ovarian or stomach cancer.	CC	CC	
CC SSX5 gene expression indicates the same cancers as SSX1, except breast	CC	CC	
CC cancer. Determining expression of SSX gene can be used to monitor	CC	CC	
CC progress of melanoma or synovial sarcoma, which is not cancer. The	CC	CC	
CC SSX-derived peptide complex stimulates proliferation of cytolytic T	CC	CC	
CC cells. This is useful for treating cancer, especially melanoma. Y78464	CC	CC	
CC to Y7968 represent specifically claimed HLA binding peptides for use in	CC	CC	
CC the method of the invention. 288452 to 288465 represent PCR primers used	CC	CC	
CC in the isolation of SSX genes in the exemplification of the present	CC	CC	
CC invention. Y78469 to Y78500, and Y79684 to Y79762 represent peptides	CC	CC	
CC derived from SSX Proteins or NY-ESO-1, which are used in the	CC	CC	
CC exemplification of the present invention.	CC	CC	
XX Sequence 9 AA;	XX	XX	
XX	DE Human secreted protein fragment encoded from gene 34.	DE	
XX	XX	XX	
KW Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour;	KW	KW	
KW neurodegenerative disorder; developmental abnormality; blood disorder;	KW	KW	
KW fetal deficiency; blood disorder; leukemia; immune system; inflammation;	KW	KW	
KW autoimmune disease; hepatic disease; renal disease; allergy; restenosis;	KW	KW	
KW ischaemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;	KW	KW	
KW cardiovascular disorder; wound healing; stroke; arthritis; obesity;	KW	KW	
KW asthma; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;	KW	KW	
XX OS Homo sapiens.	XX	XX	
RESULT 9	Db 3 aadhrql 9	Db 4 apdhqehlndvs 15	
Qy 1 AADHROL 7	Qy 1 AADHROLIS 12	Qy 1 AADHROLIS 12	
Db 4 apdhqehlndvs 15	Db 4 apdhqehlndvs 15	Db 4 apdhqehlndvs 15	
RESULT 10	RESULT 10	RESULT 10	
Y25818	Y25818 standard; Protein; 23 AA.	Y25818 standard; Protein; 23 AA.	
ID Y25818	XX	XX	
AC Y25818;	AC Y25818;	AC Y25818;	
XX DT 04-OCT-1999 (first entry)	XX DT 04-OCT-1999 (first entry)	XX DT 04-OCT-1999 (first entry)	
DE Human secreted protein fragment encoded from gene 34.	DE Human secreted protein fragment encoded from gene 34.	DE Human secreted protein fragment encoded from gene 34.	
XX	XX	XX	
Query Match 40.0%; Score 36; DB 21; Length 9;	Query Match 39.8%; Score 35; DB 13; Length 21;	Query Match 39.8%; Score 35; DB 13; Length 21;	
Best Local Similarity 100.0%; Pred. No. 3.2e+05; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 50.0%; Pred. No. 14; Mismatches 3; Indels 0; Gaps 0;	Best Local Similarity 50.0%; Pred. No. 14; Mismatches 3; Indels 0; Gaps 0;	
Matches 7; Conservative 7; Gaps 0; Indels 0; Gaps 0;	Matches 6; Conservative 3; Gaps 0; Indels 0; Gaps 0;	Matches 6; Conservative 3; Gaps 0; Indels 0; Gaps 0;	
Qy 1 AADHROL 7	Qy 1 AADHROLIS 12	Qy 1 AADHROLIS 12	
Db 4 apdhqehlndvs 15	Db 4 apdhqehlndvs 15	Db 4 apdhqehlndvs 15	
RESULT 9	RESULT 9	RESULT 9	

KW	diagnosis; prevention; melanoma; breast cancer; ovarian cancer;			
PN	prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;			
XX				
WO9938881-A1.				
05-AUG-1999.				
27-JAN-1999;	99WO-US01621-			
XX				
PR				
30-JAN-1998;	98US-0073170			
30-JAN-1998;	98US-0073159			
30-JAN-1998;	98US-0073160			
30-JAN-1998;	98US-0073161			
30-JAN-1998;	98US-0073162			
30-JAN-1998;	98US-0073164			
30-JAN-1998;	98US-0073165			
30-JAN-1998;	98US-0073167			
XX				
PA				
(HUMA -) HUMAN GENOME SCI INC.				
PI				
Carter KC, Endress GA, Feng P, Ferrie AM, Florence C;				
Florence KA, Janat F, Ni J, Rosen CA, Ruben SM;				
Soppet DR, Young P, Yu G;				
XX				
PR				
WPI; 1999-469315/39.				
N-PSDB; 200443.				
XX				
PS				
New isolated human genes and the secreted polypeptides they encode useful in, e.g. treatment of Alzheimer's				
Disclosure; Page 357: 393pp; English.				
XX				
PS				
This invention describes novel human genes (see 200410-700477) and the secreted proteins (see Y2571-Y25778) and fragments (see Y5779-Y25907) they encode. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 67 polynucleotides of the invention, based on which tissues they are most highly expressed in and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, ischaemic shock, Alzheimer's and cognitive disorders, schizophrenia, restenosis, cardiovascular disorders, wound healing, stroke, arthritis, sepsis, acne, psoriasis, transplant rejection, metabolic disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.				
XX				
CC				
Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC major histocompatibility Class II HLA-DR3 molecules, thereby stimulating proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially isolated from oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.				
CC				
Claim 4; Page 22: 49pp; English.				
XX				
PT				
Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes				
XX				
PT				
Stockert E, Jager B, Chen Y, Scanlan M, Alexander K, Old LJ;				
P1				
Gure A, Ritter G;				
XX				
PR				
17-APR-1998;	98US-0062422;			
PR				
02-OCT-1998;	98US-0165546;			
XX				
DR				
WPI; 2000-038483/03.				
XX				
PT				
Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes				
XX				
PT				
Claim 4; Page 22: 49pp; English.				
XX				
PT				
Sequence 18 AA;				
SQ				

OS Synthetic.	FT XX	/note= "any amino acid"
OS Homo sapiens.	PN WO9526983-A2.	
XX WO945954 A1.	PN	
XX 16-SEP-1999.	XX	12-OCT-1995.
PD 13-MAR-1998; 98WO-US05039.	PD	
PF 13-MAR-1998; 98WO-US05039.	XX	30-MAR-1995; 95WO-US03945.
PR 13-MAR-1998; 98WO-US05039.	XX	15-AUG-1994; 94US-0291591.
XX (EPIM-) EPIMUNE INC.	PR	31-MAR-1994; 94US-0221642.
PA Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;	PR	31-MAY-1994; 94US-0251691.
PI Hobert O, Jallal B, Kostka G, Obermeier A, Ullrich A;	PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX DR WPI; 1999-551214/46.	XX	XX Hobert O, Jallal B, Kostka G, Obermeier A, Ullrich A;
XX PT New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases -	DR	XX DR WPI; 1995-366151/47.
PT XX	XX	XX Treatment of a disease or condition characterised by abnormality in PT a signal transduction pathway - by disrupting or promoting the PT interaction in vivo
PS Claim 1; Page 27; 150pp; English.	XX	XX Example 1; Page 70; 100pp; English.
XX Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.	CC	CC R84751 and R84752 represent fragments of a GST-phospholipase C-gamma-SH3 fusion protein. This sequence was screened to see if it could be used for the treatment of a disease where there is an abnormality in a signal transduction pathway. The screening method looks for a disruption (or promotion) of the interaction between this sequence and an SH3 domain. The sequence can also be used for screening non-haematopoietic cells for a protein with an SH3 domain. The methods can be used for screening, diagnosing, and treating diseases, such as neurodegenerative or neuroproliferative disorders, or cancers.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.	CC	CC
CC They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise to risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.	CC	CC
XX Sequence 13 AA;	SQ	Query Match 33.0%; Score 29; DB 16; Length 18; Best Local Similarity 62.5%; Pred. No. 1.3e-02; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX	Qy 3 DHQLQLS 10 : : : Db 2 dyrqlela 9	Qy 3 DHQLQLS 10 : : : Db 2 dyrqlela 9
XX	RESULT 14 W96889 ID W96889 standard; peptide: 18 AA. XX AC W96889; XX	RESULT 14 W96889 ID W96889 standard; peptide: 18 AA. XX AC W96889; XX
XX	10 SRSQQ 17 : : : Db 1 stsschq 8	10 SRSQQ 17 : : : Db 1 stsschq 8
XX	DE R84751 ID R84751 Standard; peptide; 18 AA. XX AC R84751; XX DT 21-MAY-1996 (first entry)	DE ApoB-100 nuclear localisation signal sequence, residues 2228-2245. ID Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; KW non-small cell lung carcinoma; diabetes; arteriosclerosis. XX Homo sapiens XX WO956938-A1. XX
XX	DE GST-phospholipase C-gamma-SH3 fusion protein fragment #1. XX Ribonuclease; DYN domain; signal transduction; SH3 domain; therapy; KW neurodegenerative disorder; neuroproliferative disorder; cancer; dynamin. XX OS Synthetic. XX Key Location/Qualifiers FH Misc-difference 10 FT	DE ApoB-100 nuclear localisation signal sequence, residues 2228-2245. ID Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; KW non-small cell lung carcinoma; diabetes; arteriosclerosis. XX Homo sapiens XX WO956938-A1. XX
XX	PR 14-MAY-1998; PR 13-JUN-1997; XX 98WO-US11927. PA (BAYU) BAYLOR COLLEGE MEDICINE.	DE ApoB-100 nuclear localisation signal sequence, residues 2228-2245. ID Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; KW apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; KW nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; KW non-small cell lung carcinoma; diabetes; arteriosclerosis. XX Homo sapiens XX WO956938-A1. XX

XX Guevara JG, Hoogeveen RC, Moore JP; PT fusion proteins and ob monomer fusion proteins, useful, e.g. for
 XX PI; 1999-070331/06. PT treating obesity or diabetes
 XX PT Composition comprising nucleic acid bound to LDL or VLDL lipoprotein
 - used for delivering nucleic acid to cells for gene therapy and CC
 antisense treatment CC fragment based on residues 148-167, which can be used as an antigen
 XX PT in the preparation of antibodies (Ab) against the rat ob CC protein. The Ab can be used for detection, assays and CC purifications.
 XX PS; Page 130pp; English.
 XX Example 8; Page 130pp; English.
 XX The present sequence is a modified rat obese (ob) protein
 CC fragment based on residues 148-167, which can be used as an antigen
 CC in the preparation of antibodies (Ab) against the rat ob CC protein. The Ab can be used for detection, assays and CC purifications.
 XX SQ Sequence 20 AA;
 CC W96878-97 represent nuclear localisation signal sequence derived from
 CC human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein
 CC component of very low density lipoproteins (VLDL), intermediate density
 CC lipoprotein (IDL), low density lipoproteins (VLDL) and lipoprotein a.
 CC The present sequence can be used in the composition of the invention.
 CC The specification describes a composition that comprises LDL and
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.
 CC in vivo or in vitro, for delivering nucleic acids to eukaryotic cells,
 CC antisense molecule (or ribozyme). Specifically, they are used for gene
 CC therapy of cancers (particularly non-small cell lung carcinoma),
 CC diabetes, cystic fibrosis and arteriosclerosis.
 XX Sequence 18 AA;
 CC W96878-97 represent nuclear localisation signal sequence derived from
 CC human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein
 CC component of very low density lipoproteins (VLDL), intermediate density
 CC lipoprotein (IDL), low density lipoproteins (VLDL) and lipoprotein a.
 CC The present sequence can be used in the composition of the invention.
 CC The specification describes a composition that comprises LDL and
 CC apolipoproteins for the binding and in vivo transport of nucleic acids.
 CC in vivo or in vitro, for delivering nucleic acids to eukaryotic cells,
 CC antisense molecule (or ribozyme). Specifically, they are used for gene
 CC therapy of cancers (particularly non-small cell lung carcinoma),
 CC diabetes, cystic fibrosis and arteriosclerosis.
 XX Sequence 18 AA;
 Query Match 33.0%; Score 29; DB 17; Length 20;
 Best Local Similarity 53.8%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 QLQLSISSSCQLQQL 18
 :|||:
 Db 2 rlqqlslqdlqlqql 14
 Search completed: May 8, 2001, 15:07:07
 Job time: 223 sec

RESULT 15
 W11227 ID W11227 standard; Peptide; 20 AA.
 XX AC W11227;
 XX DT 17-JUN-1997 (first entry)
 XX DE Modified rat obese (ob) protein fragment (1).
 XX KW Modified; rat; obese; ob; fragment; antigen; antibody;
 XX KW detection; assay; purification.
 OS Rattus rattus.
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "acylated"
 Peptide 1..20
 FT /note= "residues 148-167 of rat ob protein"
 XX PN W0963156-A1.
 XX PD 10-OCT-1996.
 XX PF 05-APR-1996; 96WO-US04909.
 XX PR 06-APR-1995; 95US-0419598.
 XX PA (AMYL-) AMYLIN PHARM INC.
 PI Albrandt KA, Beasley N, Beidler DE, Chun M, Janes SM;
 PI Park DM, Phelps JL, Prickett KS, Rink TJ, Sierzega ME;
 XX DR 1996-464965/46.
 XX PT Modified obese (ob) gene prods. - comprising ob dimers, ob dimer

Tue May 8 15:56:44 2001

us-09-165-546a-8.rag

Page 9

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:08:18 ; Search time 68.24 Seconds
(Without alignments)
18.127 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHQQLSISSCQQL 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters:

4929

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : PIR_67;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	36.4	23	S72535	probable acr-2 reg hypothetical MTCOI
2	30	34.1	24	S09363	collagen alpha 2(I)
3	28	31.8	23	S31210	arginine-tRNA lig
4	25	28.4	20	A35857.	blaz protein - Sta
5	24	27.3	16	S3444	chorion class A pr
6	24	27.3	17	S05917	homodomain protein
7	24	27.3	23	S60570	hemoglobin ATR - t
8	24	27.3	24	S01808	B144 protein A - m
9	23	26.1	14	I49114	lipid transfer pro
10	23	26.1	15	S28873	high-cysteine chor
11	23	26.1	17	B2219	trp leader peptide
12	23	26.1	17	A28834	actin-related prot
13	23	26.1	21	S45550	40K iron-repressed
14	23	26.1	22	T1833	NADH dehydrogenase
15	23	26.1	24	T17073	C1-inhibitor - hum
16	22	25.0	14	I54284	major fat-globule
17	22	25.0	15	D48394	chorion class A pr
18	22	25.0	17	S05913	vonmulin A (EC 3.4
19	22	25.0	20	A60489	fibrinogenolytic p
20	22	25.0	21	G64364	hypothetical prote
21	22	25.0	21	H64640	hypothetical prote
22	22	25.0	21	H71858	homodomain protei
23	22	25.0	23	S60564	gene rRNP-A protei
24	21	23.9	12	I57678	T cell receptor al
25	21	23.9	14	PH1806	fibrinolysis elonga
26	21	23.9	18	S63487	L-2,4-diaminobuty
27	21	23.9	18	S59490	photosystem I 8.0k
28	21	23.9	19	A44854	translating elonga
29	21	23.9	19	PQ0678	T cell receptor be

30	21	23.9	20	2	B53875
31	21	23.9	20	2	S14161
32	21	23.9	21	2	S68971
33	21	23.9	21	2	A53630
34	21	23.9	22	2	A41833
35	21	23.9	22	2	F84018
36	21	23.9	24	2	S30923
37	21	23.9	24	2	A58999
38	21	23.9	25	2	D47689
39	20	22.7	6	2	S71349
40	20	22.7	13	2	PT0305
41	20	22.7	14	2	PH1321
42	20	22.7	15	2	PT0096
43	20	22.7	17	2	S05923
44	20	22.7	17	2	S57519
45	20	22.7	18	2	A41877

ALIGNMENTS

RESULT 1	S7235	probable acr-2 regulatory leader protein - Neurospora crassa
C;Species:	Neurospora crassa	
C;Date:	19-Mar-1998	#sequence_revision 17-Apr-1998 #text_change 21-Jul-2000
C;Accession:	S72535	
R;Akiyama, M.; Nakashima, H.		
Biochim. Biophys. Acta 1307, 187-192, 1996		
A;Title: Molecular cloning of the acr-2 gene which controls acriflavine sensitivity 1		
A;Reference number: S72535; MUID:96283814		
A;Accession: S72535		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-23 <RKI>		
A;Cross-references: EMBL:D45893; PIDN:BAA08306.1; PID:91754593; NID:91754593; PIDN:BA08306.1; PID:g1754594		

Query	Match	36.4%; Score 32; DB 2; Length 23;
Best Local Similarity 50.0%; Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
Qy	5 ROLLSISSC 14	
Db	11 RMIREVSSC 20	
RESULT 2	S09363	hypothetical MTCOI/MTCYB mutant fusion protein - human mitochondrion (fragment)
C;Species:	mitochondrion Homo sapiens (man)	
C;Date:	21-Nov-1993	#sequence_revision 14-Aug-1997 #text_change 20-Apr-2000
C;Accession:	S09363	
R;Poulton, J.; Deadman, M.E.; Gardiner, R.M.		
Nucleic Acids Res. 17, 10223-10229, 1989		
A;Title: Tandem direct duplications of mitochondrial DNA in mitochondrial myopathy: a reference number: S09363; MUID:90098864		
A;Molecule type: DNA		
A;Residues: 1-24 <POU>		
C;Comment: This is the hypothetical translation of a sequence believed to result from C;Genetics:		
A;Gene: MTCOI/MTCYB		
A;Genomic: mitochondrion		
A;Genetic code: SGCI		
C;Keywords: fusion protein; mitochondrion		
F;1-24/Region: cytochrome-c oxidase chain I		
F;5-24/Region: Cytochrome b (+2 frame shifted)		
Query	Match	34.1%; Score 30; DB 4; Length 24;
Best Local Similarity 44.4%; Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 1;		

A; Residues: 1-16 <WAN>
 A; Cross-references: EMBL:M62650
 A; Experimental source: strain RN11
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library. September 199
 C; Genetics:
 A; Gene: blaZ
 A; Genome: plasmid pI258

RESULT 3
 S31210 collagen alpha 2(I) chain precursor - rat (fragment)
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C; Accession: S31210
 R; Guenette, D.K.; Ritzenthaler, J.D.; Foley, J.; Jackson, J.D.; Smith, B.D.
Biochem. J. 283, 639-703, 1992
 A; Title: DNA methylation inhibits transcription of procollagen alpha-2(I) promoters.
 A; Reference number: S31110; MUID:9227266
 A; Accession: S31210
 A; Status: translation not shown
 A; Molecule type: DNA
 A; Residues: 1-23 <SUE>
 A; Cross-references: EMBL:X66209; NID:955974; PID:CAA46960_1; PID:g55975
 C; Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
 C; Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix

Query Match Score 28; DB 2; Length 23;
 Best Local Similarity 55.6%; Pred. No. 1.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY | LQLSSCL 15
 Db 11 LLLAVTSCL 19

RESULT 4
 A35857 arginine--tRNA ligase (EC 6.1.1.19) - rat (fragment)
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 14-Nov-1997
 C; Accession: A35857
 R; Sivaram, P.; Deutscher, M.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 3665-3669, 1990
 A; Title: Existence of two forms of rat liver arginyl-tRNA synthetase suggests channeling
 A; Reference number: A35857; MUID:90251617
 A; Accession: A35857
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-20 <SIV>
 C; Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match Score 25; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.6e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY | LSISSCLQQL 18
 Db 2 INNSXLQEL 11

RESULT 5
 S34444 blaZ protein - *Staphylococcus aureus* plasmid pI258 (fragment)
 C; Species: *Staphylococcus aureus*
 C; Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 07-May-1999
 C; Accession: S34444
 R; Wang, P.Z.; Projan, S.J.; Novick, R.P.
Nucleic Acids Res. 19, 4000, 1991
 A; Title: Nucleotide sequence of beta-lactamase regulatory genes from staphylococcal plas
 A; Reference number: S34444; MUID:91319567
 A; Accession: S34444
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA

A; Residues: 1-16 <WAN>
 A; Cross-references: EMBL:M62650
 A; Experimental source: strain RN11
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library. September 199
 C; Genetics:
 A; Gene: blaZ
 A; Genome: plasmid pI258

Query Match Score 27.3%; DB 2; Length 16;
 Best Local Similarity 71.4%; Pred. No. 5.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY | RQLQLST 11
 Db 6 KQLQLKT 12

RESULT 6
 S05917 chorion class A protein L4 precursor - silkworm (fragment)
 C; Species: *Bombyx mori* (silkworm)
 C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Aug-1999
 C; Accession: S05917
 R; Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Rafatos, F.C.
J. Mol. Biol. 209, 1-19, 1989
 A; Title: Gene evolution and regulation in the chorion complex of *Bombyx mori*. Hybrid
 A; Reference number: S05913; MUID:90040707
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-17 <SPO>
 A; Cross-references: EMBL:X15560; NID:95781; PID:CAA33571_1; PID:g5782
 A; Note: this sequence was submitted to the EMBL Data Library, Jun-1982
 C; Genetics:
 A; Map Position: 2
 C; Superfamily: chorion class A protein pc292

Query Match Score 27.3%; DB 2; Length 17;
 Best Local Similarity 45.5%; Pred. No. 5.8e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY | IQLSRSCLQO 17
 Db 7 LLLCVQACLIQ 17

RESULT 7
 S60570 homeodomain protein hrox8 - California red abalone (fragment)
 C; Species: *Haliotis rufescens* (California red abalone)
 C; Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
 C; Accession: S60570
 R; Degnan, B.M.; Morse, D.E.
Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
 A; Title: Identification of eight homeobox-containing transcripts expressed during lar
 A; Reference number: S60564; MUID:93372986
 A; Accession: S60570
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-23 <DEG>
 C; Superfamily: unassigned homeobox proteins; homeobox homology
 C; Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match Score 27.3%; DB 2; Length 23;
 Best Local Similarity 23.1%; Pred. No. 8e+02;
 Matches 3; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY | RQLQLSTSQLQ 17

Db 9 RERIAHTLCLE 21

RESULT 8

SO1808 hemoglobin MII - tube worm (*Lamellibrachia* sp.) (fragment)

C;Species: *Lamellibrachia* sp.

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 04-Mar-2000

C;Accession: SO1808

R;Suzuki, T.; Ohta, S.

Biochem. J. 255, 541-545, 1988

A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably similar to those of sea lamprey and hagfish haemoglobins

A;Reference number: SO1807; MUID:89076216

A;Accession: SO1808

A;Molecule type: protein

A;Residues: 1-24 <S02>

C;Superfamily: globin; globin homology

C;Keywords: oxygen carrier

Query Match 27.3%; Score 24; DB 2; Length 24;

Best Local Similarity 57.1%; Pred. No. 8.3e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULTS 9

Qy 3 DHQLQL 9

 | : | : |

Db 9 DREMQL 15

RESULT 9

I49514 B144 protein A - mouse (fragment)

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

R;Tsuge, I.; Shen, F.

Immunogenetics 26, 378-380, 1987

A;Title: A gene in the H-2S: H-2D interval of the major histocompatibility complex which encodes a leader peptide - *Corynebacterium glutamicum*

A;Reference number: I49514; MUID:88031493

A;Accession: I49514

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-14 <RES>

A;Cross-references: GB:MI1817; NID:9192097; PIDN:AAA37272.1; PID:9192098

Query Match 26.1%; Score 23; DB 2; Length 14;

Best Local Similarity 40.0%; Pred. No. 7.2e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

RESULTS 10

Qy 9 LSISSSCLQQ 18

 | : | : |

Db 2 LDLQACSQSL 11

RESULT 10

S28873 Lipid transfer protein Cw41) - maize (fragment)

C;Species: Zea mays (maize)

C;Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

R;Molina, A.; Segura, A.; Garcia-Olmedo, F.

FEBS Lett. 316, 119-122, 1993

A;Title: Lipid transfer proteins (nsLTPs) from barley and maize leaves are potent inhibitors of seedling growth

A;Reference number: S28871; MUID:93131027

A;Accession: S28873

A;Molecule type: protein

A;Residues: 1-15 <MOL>

A;Experimental source: etiolated leaf, cultivar INIA 1986

C;Keywords: lipid transport

Query Match 26.1%; Score 23; DB 2; Length 15;

Best Local Similarity 40.0%; Pred. No. 7.7e+02; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 6 QLOQSISSCL 15

 | : | : |

Db 6 QVSXAIAPCL 15

RESULT 11

B23219 high-cysteine chorion protein A 13 - silkworm (fragment)

C;Species: *Bombyx mori* (silkworm)

C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 21-Jul-2000

C;Accession: B23219

R;Rodakis, G.C.; Lecanidou, R.; Bickbush, T.H.

J. Mol. Evol. 20, 265-273, 1984

A;Title: Diversity in a chorion multigene family created by tandem duplications and a frameshift mutation

A;Reference number: A92960; MUID:85083111

A;Accession: B23219

A;Molecule type: DNA

A;Residues: 1-17 <R0D>

A;Cross-references: GB:X01068; NID:95752; PIDN:CAB57790.1; PID:96015486

C;Genetics:

A;Introns: 17/3

C;Supertamily: chorion class A protein pc292

Query Match 26.1%; Score 23; DB 2; Length 17;

Best Local Similarity 45.5%; Pred. No. 8.8e+02; Mismatches 5; Indels 0; Gaps 0;

Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 7 LQLSISSCLQQ 17

 | : | : |

Db 7 LILCVQGCCLIQ 17

RESULT 12

A29834 trp leader Peptide - *Corynebacterium glutamicum*

C;Species: *Corynebacterium glutamicum*

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999

C;Accession: A29834; A24723; A29458; SI3087; A48967

R;Matsuji, K.; Miwa, K.; Sano, K.

J. Bacteriol. 169, 5330-5332, 1987

A;Title: Two single-base-pair substitutions causing desensitization to tryptophan

A;Content: not compared with conceptual translation

A;Residues: 1-17 <MAT>

A;Cross-references: GB:MI7892; NID:9144101; PIDN:AAB59110.1; PID:91129101

R;Matsuji, K.; Ohtsubo, E.

Nucleic Acids Res. 14, 10113-10114, 1986

A;Title: Complete nucleotide and deduced amino acid sequences of the *Brevibacterium* 1

A;Content: B. lactofermentum

A;Accession: A29834

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-17 <MAT>

A;Cross-references: GB:MI7892; NID:9144101; PIDN:AAB59110.1; PID:91129101

R;Matsuji, K.; Ohtsubo, E.

Nucleic Acids Res. 14, 10113-10114, 1986

A;Title: Complete nucleotide and deduced amino acid sequences of the *Brevibacterium* 1

A;Content: B. lactofermentum

A;Accession: A29834

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-17 <CMA2>

A;Cross-references: GB:X04960; NID:939591; PIDN:CAA28632.1; PID:9580785

R;Cano, K.; Matsui, K.

Gene 53, 191-200, 1987

A;Title: Structure and function of the *trp* operon control regions of *Brevibacterium* 1

A;Content: B. lactofermentum

A;Accession: A29438

A;Molecule type: DNA

A;Residues: 1-17 <SAN>

A;Cross-references: GB:X04960; NID:939591; PIDN:CAA28632.1; PID:9580785

R;Heery, D.M.; Duncan, L.K.

Nucleic Acids Res. 18, 7138, 1990

A;Title: Nucleotide sequence of the *Corynebacterium glutamicum* *trpE* gene

A; Reference number: S13087; MUID:91088299
 A; Accession: S13087
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-17 <HER>
 A; Cross-references: EMBL:X55994; NID:940521; PIDN:CAA39466..1; PID:9580992
 A; Cross-references: GB:S59299; NID:g299877; PIDN:AAB26395..1; PID:g299878
 A; Experimental source: ATCC 21850
 A; Note: sequence extracted from NCBI backbone (NCBIN:130455, NCBIPI:130456)
 C; Genetics:
 A; Gene: trpL
 A; Start codon: GTG
 C; Superfamily: unassigned leader peptides
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-13 <HER>
 A; Cross-references: GB:S59299; NID:g299877; PIDN:AAB26395..1; PID:g299878
 A; Note: sequence extracted from NCBI backbone (NCBIN:130455, NCBIPI:130456)
 C; Genetics:
 A; Gene: trpL
 A; Start codon: GTG
 C; Superfamily: unassigned leader peptides

Query Match 26.1%; Score 23; DB 2; Length 22;
 Best Local Similarity 14.3%; Pred. No. 1.2e+03;
 Matches 5; Indels 0; Gaps 0;

QY 4 HROLQLSISSSCQQ 17
 |:: ::| :|
 Db 9 HKEAAVAVAKAFAEQ 22

RESULT 15

T17073
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Chamaeleo fischeri mitochondri
 C; Species: mitochondron Chamaeleo fischeri
 C; Date: 15-Oct-1999 #sequence_change 15-Oct-1999 #text_change 11-Jan-2000
 C; Accession: T17073
 R; Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
 J. Mol. Evol. 44, 660-674, 1997
 A; Title: Evolutionary shifts in three major structural features of the mitochondrial
 A; Reference number: Z18674; MUID:9715309
 A; Accession: T17073
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-24 <MAC>
 C; Superfamily: NADH dehydrogenase (ubiquinone) chain 1
 C; Cross-references: EMBL:U82688; NID:g3603112; PID:g3603113; PIDN: AAC62273.1
 C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 26.1%; Score 23; DB 2; Length 24;
 Best Local Similarity 14.4%; Pred. No. 1.3e+03;
 Matches 3; Indels 0; Gaps 0;

QY 7 LOLSISSCL 15
 |:: :|
 Db 3 LPLTLMCL 11

Search completed: May 8, 2001, 15:08:19
 Job time: 290 sec

RESULT 13

S46550
 actin-related protein - chicken (fragments)
 C; Species: Gallus gallus (chicken)
 C; Date: 12-Sep-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C; Accession: S46550
 R; Lees-Miller, J.P.; Halfman, D.M.; Schroer, T.A.
 Nature 359, 244-246, 1992
 A; Title: A vertebrate actin-related protein is a component of a multisubunit complex involved in
 A; Reference number: S29089; MUID:92408781
 A; Accession: S46550
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-21 <LEE>

Query Match 26.1%; Score 23; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 2; Indels 0; Gaps 0;

QY 1 AADPHRLQ 8
 |:: :|
 Db 9 AEEHRKAQ 16

RESULT 14

B41833
 40K iron-repressed periplasmic protein - Haemophilus influenzae (strain PAK12085) (fragment)
 C; Species: Haemophilus influenzae
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Jan-2000
 C; Accession: B41833
 R; Harkness, R.E.; Chong, P.; Klehn, M.H.
 J. Bacteriol. 174, 2428-2430, 1992
 A; Title: Identification of two iron-repressed periplasmic proteins in Haemophilus influenzae
 A; Reference number: A41833; MUID:92210482
 A; Accession: B41833
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-22 <HAR>
 C; Superfamily: sfuA protein

correct score:
sequence:
direct score:
AACDHROTISTSSCQLN, 18

Scoring table: BLOSUM62 Alignments

searched : 9345 seqs, 34255486 residues
RESULT 1 SYR_PAT -

Total number of hits satisfying chosen Parameters: 1423

maximum DB seq length: 25
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE ARGINYL-tRNA SYNTHETASE (EC 6.1.1.19) (ARGININE--tRNA LIGASE) (ARGRS)

SUMMARIES
Sivaram P., Deutscher M.P.
Existence of two forms of rat liver arginyl-tRNA synthetase suggests

	Query	Match	Score	DB	Length
1	monotone	monotone	100.00	DB1	20
2	similarity	similarity	100.00	DB2	20
3	best	best	100.00	DB3	20
4	similarity	similarity	100.00	DB4	20
5	length	length	100.00	DB5	20
6	DB1	DB1	100.00	DB6	20
7	DB2	DB2	100.00	DB7	20
8	DB3	DB3	100.00	DB8	20
9	DB4	DB4	100.00	DB9	20
10	DB5	DB5	100.00	DB10	20

TISON	CYPCA	18	18
FAR	MYTBD	18	20.5
TISON	CYPCA	18	20.5
FAR	MYTBD	18	20.5
TISON	CYPCA	19	9
FAR	MYTBD	19	10
TISON	CYPCA	2	ININSXQEL
FAR	MYTBD	2	Db

		STANDARD;	PRR;	17 Å.
C02H3_BOMMO	ID	P20/29;		
P02H20_staphylococ	AC			
P02H20_pseudomonas				
Q02H3_staphylococ				
YHOR_PSPW				
PHIC_STAN				
18	20.5	16	1	
18	20.5	19	1	
24	18	18	1	
25	18	20.5	1	

OC Bombycoidea; Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1] SEQUENCE FROM N.A.; PubMed=6439880;
 RX MEDLINE=85083111; PubMed=6439880;
 RA Rodakis G.C.; Lecanidou P.; Eickbush T.H.;
 RT "Diversity in a chorion multigene family created by tandem
 duplications and a putative gene conversion event.";
 RL J. Mol. Evol. 20:265-273(1994).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF MANY FROM THE EGGSHELL OF THE
 SILK MOTH.
 CC -!- SIMILARITY: MEMBER OF THE ALPHA-BRANCH OF CHORION PROTEIN TO WHICH
 BELONG CLASSES A, CA AND HCA.

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CC DR EMBL: X01068; CAB7790_1; -;
 DR PIR: B2219; B23219;
 KW Egsshell; Chorion; Repeat; Multigene family; Signal.
 FT SIGNAL 1 >17
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1913 MW; 5E634508c5355c9C CRC64;

Query Match Score 23; DB 1; Length 17;
 Best Local Similarity 45.5%; Pred. No. 3 3e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 LQLSISSCIQQ 17
 Db 7 LLICvQgCLIQ 17

RESULT 3
 LPW_BRELA ID LPW_BRELA STANDARD; PRT; 17 AA.
 AC P065256;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DE TRP OPERON LEADER PEPTIDE.
 GN TRPL.
 OS Brevibacterium glutamicum (Brevibacterium flatum) Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae.
 OC NCBI_TaxID=92707; 1718;
 OX
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES=B.lactofermentum;
 RX MEDLINE=871171512; PubMed=3808947;
 RT "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon.";
 RT Nucleic Acids Res. 14:10113-10114(1985).
 RN [2] SEQUENCE FROM N.A.
 RP SPECIES=B.lactofermentum;
 RX MEDLINE=88032866; PubMed=3667535;
 RA Matsui K.; Miwa K.; Sano K.;
 RT "Two single-base-pair substitutions causing desensitization to trypotophan feedback inhibition of anthranilate synthase and enhanced expression of tryptophan genes of Brevibacterium lactofermentum.";
 RT J. Bacteriol. 169:5330-5332(1987).
 RN [3] SEQUENCE FROM N.A.
 RP SPECIES=B.lactofermentum;

RX MEDLINE=87277409; PubMed=3609747;
 RA Sano K.; Matsui K.;
 RT "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
 RL Gene 53:191-200(1987).
 RN [4] SEQUENCE FROM N.A.
 RC SPECIES=C glutamicum; STRAIN=ATCC 13059 / AS019;
 RX MEDLINE=91088299; PubMed=2263476;
 RA Heery D.M.; Duncan L.K.;
 RT "Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
 RL Nucleic Acids Res. 18:7138-7138(1990).
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS OF TRYPTOPHAN.

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CC DR EMBL: X04960; CAA28622_1;
 DR EMBL: M17892; AAB59110_1;
 DR EMBL: M16663; -; NOT_ANNOTATED_CDS.
 DR EMBL: X55934; CAA39466_1;
 DR PIR: A29458; A29458.
 DR PIR: A29834; A29834.
 DR PIR: A24723; A24723.
 DR PIR: S13087; S13087.
 KW Tryptophan biosynthesis; Leader peptide.
 SQ SEQUENCE 17 AA; 2112 MW; 74c7E794DAAE56B CRC64;

Query Match Score 23; DB 1; Length 17;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SSCLQQ 17
 Db 3 NSCLSQ 8

RESULT 4
 PYRB_PSEFL ID PYRB_PSEFL STANDARD; PRT; 19 AA.
 AC P56585;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TRANSCARBAMYLASE (EC 2.1.3.2) (ASPARTATE PYRB).
 DE DE
 GN Pseudomonas fluorescens.
 OS Bacteria: Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 RN [1] Pseudomonas fluorescens.
 RN SEQUENCE.
 RT Subunit structure of a class A aspartate transcarbamoylase from Pseudomonas fluorescens.";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:9818-9822(1993).
 RL -!- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE = ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.
 CC CC
 CC -!- PATHWAY: SECOND STEP IN PYRIDINE BIOSYNTHESIS.
 CC CC
 CC -!- SUBUNIT: HETERODODECAMER OF 6 ACTIVE PYRB SUBUNITS.
 CC CC
 CC -!- CATALYTIC PYRC' SUBUNITS.
 CC CC
 CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 DR InterPro; IPR002029; -.

DR	PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.	OX	NCBI_TaxID=1931;
KW	pyrimidine biosynthesis; transferase.	RN	[1]
FT	NON_TER 19 19	RP	SEQUENCE, AND STRUCTURE BY NMR.
SQ	SEQUENCE 19 AA; 2099 MW; 7F9B77FF83B59E21 CRC64;	RX	PUBMED=8286361;
Query Match	Score 23; DB 1; Length 19;	RA	MEDLINE=4114512; PubMed=8286361;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;	1; Mismatches 5; Indels 0; Gaps 0;	RA	Frechet D., Guittot J.-D., Herman F., Faucher D., Helynck G.,
Matches 6; Conservative		RA	Moegier du Sorbier B., Ridoux J.P., James-Surcouf E., Vuilloragne M.;
Qy 5 RQLQLSISSCQ 16		RT	"Solution structure of RP 71955, a new 21 amino acid tricyclic peptide active against HIV-1 virus."
Db 8 RPLQINAQGQLQ 19		RT	Biochemistry 33:42-50(1994).
RESULT 5		RL	-1- FUNCTION: ACTIVE AGAINST HIV-1 VIRUS.
ANCR_AGKBI	STANDARD; PRT; 20 AA.	CC	-1- PTM: THERE IS AN AMIDE BOND BETWEEN CYS-1 AND ASP-9.
ID	ANCR_AGKBI	DR	PDB; 1RPB; 30-APR-94.
AC	P3588;	DR	PDB; 1RPC; 30-APR-94.
DT	01-FEB-1994 (Rel. 28, Created)	KW	Antiviral; 3D-structure.
DT	01-FEB-1994 (Rel. 28, Last sequence update)	FT	DISULFID 1 13
DT	01-NOV-1995 (Rel. 32, Last annotation update)	FT	DISULFID 7 19
DE	ANCRD (EC 3.4.21.74) (VENOMBIN A) (PROTEIN C ACTIVATOR) (ACC-C)	FT	STRAND 2 2
DE	(FRAGMENT).	FT	TURN 11 12
OS	Agkistrodon bilineatus (Cantil) (Tropical moccasin).	FT	STRAND 15 15
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	SEQUENCE 21 AA; 2186 MW; EF94FAA21634FF91 CRC64;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;	FT	DISULFID 1 13
OC	Viperidae; Crotalinae; Agkistrodon.	FT	DISULFID 7 19
OX	NCBI_TaxID=8718;	FT	STRAND 2 2
RN	[1]	FT	TURN 11 12
RP	SEQUENCE.	FT	STRAND 15 15
RC	TISSUE=Venom; MEDLINE=90150102; PubMed=2385829;	FT	SEQUENCE 21 AA; 2186 MW; EF94FAA21634FF91 CRC64;
RX	RA	FT	DISULFID 1 13
RA	Nakagaki T., Kazim A.L., Kisiel W.; Isolation and characterization of a protein C activator from tropical moccasin venom.	FT	DISULFID 7 19
RT	"Isolation and characterization of a protein C activator from tropical moccasin venom."	FT	STRAND 2 2
RT	Thromb. Res. 58:593-602 (1990).	FT	TURN 11 12
RL	CC	FT	STRAND 15 15
CC	-1- FUNCTION: THROMBIN-LIKE SNAKE VENOM SERINE PROTEASE CLEAVES FIBRINOPEPTIDES AM, AO, AND AY; THE ABERRANT FIBRINOGEN IS THEN INCAPABLE OF BEING CROSS-LINKED, FORMING EASILY DISPERSIBLE CLOTS.	FT	SEQUENCE 21 AA; 2186 MW; EF94FAA21634FF91 CRC64;
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. SNAKE VENOM SUBFAMILY.	FT	DISULFID 1 13
CC	PIR: A60489; A60489.	FT	DISULFID 7 19
DR	MEROPS; S01.178;	FT	STRAND 2 2
DR	INTERRO; IPR001254;	FT	TURN 11 12
DR	PROSITE; PS00134; TRYPSIN HIS; PARTIAL.	FT	STRAND 15 15
DR	PROSITE; PS00135; TRYPSIN_SER; PARTIAL.	FT	SEQUENCE 21 AA; 2186 MW; EF94FAA21634FF91 CRC64;
KW	Hydrolase; Serine protease; Venom; Glycoprotein.	FT	DISULFID 1 13
FT	NON_TER 20 20	FT	DISULFID 7 19
SQ	SEQUENCE 20 AA; 2191 MW; 6E99FB4CC53EEF1 CRC64;	FT	STRAND 2 2
Query Match	Score 22; DB 1; Length 20;	FT	TURN 11 12
Best Local Similarity 57.1%; Pred. No. 6e+02;	1; Mismatches 2; Indels 0; Gaps 0;	FT	STRAND 15 15
Matches 4; Conservative		FT	SEQUENCE 21 AA; 2186 MW; EF94FAA21634FF91 CRC64;
Qy 3 DHQLQQL 9		FT	DISULFID 1 13
Db 11 EHRSFL 17		FT	DISULFID 7 19
RESULT 6		FT	STRAND 2 2
ID	RP71_STRSQ	FT	SEQUENCE 25 AA; 2746 MW; 1AAA0CA722EE3DDA CRC64;
AC	P37046;	FT	DISULFID 1 13
DT	01-JUN-1994 (Rel. 29, Created)	FT	DISULFID 7 19
DT	01-FEB-1995 (Rel. 31, Last sequence update)	FT	DISULFID 1 13
DB	RP 71955;	FT	DISULFID 1 13
OS	Streptomyces sp. (strain SP9440).	FT	DISULFID 1 13
OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Streptomyces.	FT	DISULFID 1 13
OC	Actinomycetales; Streptomycineae; Streptomyctaceae; Streptomyces.	FT	DISULFID 1 13
Query Match	Score 21; DB 1; Length 25;	FT	DISULFID 1 13
Best Local Similarity 50.0%; Pred. No. 1.2e+03;	3; Mismatches 2; Indels 0; Gaps 0;	FT	DISULFID 1 13
Matches 5; Conservative		FT	DISULFID 1 13
Qy 4 HROLQLSS 13		FT	DISULFID 1 13
Db 13 NRQLNLGNS 22		FT	DISULFID 1 13

RESULT 8
 OXT_RAICL STANDARD; PRT; 9 AA.
 ID RAICL
 AC PA2994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE GLDMTOIN.
 OS Raja clavata (Thornback ray);
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 Elasmobranchii; Squalae; Hypnosqualea; Pristiorajea; Batoidea;
 Rajiformes; Rajidae; Raja.
 NCBI_TaxID=7781;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=66123415; PubMed=5880565;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Phylogeny of neuromodulatory peptides: isolation of a new hormone,
 glutamotocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
 the ray (Raja clavata).";
 RT BioPhys. Acta 107:393-396 (1955).
 CC !- FUNCTION: ANTIIDIURETIC HORMONE.
 CC !- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro; IPR005981;
 PRIM; PF00220; hormone; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SEQUENCE 9 AA; 984 MW; 17E9C76EB45B04B CRC64;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=87185451; PubMed=3105581;
 RA Herbert P. N., Bausserman L. L., Lynch K. M., Saritelli A. L.,
 RA Kantor M. A., Nicolosi R. J., Shulman R. S.;
 RT Homologues of the human C and A apolipoproteins in the Macaca
 fascicularis (cynomolgus monkey).";
 RL Biochemistry 26:1457-1463 (1987).
 CC !- FUNCTION: APPEARS TO MODULATE THE INTERACTION OF APOE WITH BETA-
 DE MIGRATION; VLDL AND INHIBIT BINDING OF BETA-VLDL TO THE LDL
 PRO. RECEPTOR-RELATED PROTEIN.
 CC !- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC !- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC !- MISCELLANEOUS: APO-C1 MAKES UP ABOUT 10% OF THE PROTEIN OF THE
 VLDL (VERY LOW DENSITY LIPOPROTEIN) & 2% OF THAT OF HDL (HIGH
 DENSITY LIPOPROTEIN).
 CC !- SIMILARITY: BELONGS TO THE APOC1 FAMILY.
 CC PIR; C26627; C26627.
 DR HSSP; P02654; IOPP.
 KW Plasma; Lipid transport; VLDL.
 FT NON_TER 22 22
 SEQUENCE 22 AA; 2349 MW; 4E478A03C91EA914 CRC64;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ltr2;
 RX MEDLINE=93308095; PubMed=8331535;
 RA Roland K.L., Martin L.R., Esther C.R., Spitznagel J.K.;
 RT "Spontaneous pmra mutants of Salmonella typhimurium ltr2 define a new
 two-component regulatory system with a possible role in virulence.";
 RL J. Bacteriol. 175:4154-4164 (1993).
 CC !- FUNCTION: STRETCH-INACTIVATED PROLINE/BETAINE TRANSPORTER. PROP IS
 BOTH AN OSMORESENSE AND AN OSMOREGULATOR WHICH IS AVAILABLE TO
 PARTICIPATE EARLY IN THE BACTERIAL OSMOREGULATORY RESPONSE.
 CC MEDiates THE ACTIVE ACCUMULATION OF SOLUTES SUCH AS PROLINE,
 GLYCINE BETaine, STACHYDRINE, PIPOCOLIC ACID, EUCOINE AND TAURINE.
 CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC !- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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 CC

RESULT 11
 ID CH60_BOVIN STANDARD; PRT; 22 AA.
 AC P1081;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DR 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP60) (60 KDA CHAPERONIN), DE (CPN60), (HEAT SHOCK PROTEIN 60) (HSP 60) (MITOCHONDRIAL MATRIX PROTEIN 60) (FRAGMENT).
 RXN HSPD1 OR HSP60.
 OS Bos taurus (Bovine).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Bovinae; Bos.
 OC NCBITaxonID=9913;
 RN [1]
 RP SEQUENCE.
 TISSUE_Adrenal gland;
 MEDLINE=93208180; PubMed=8096152;
 RA Dai Z., Lackland H., Stein S., Li Q., Radziewicz R., Williams R., Signal L.H.;
 RT "Molecular mimicry in Lyme disease: monoclonal antibody H9724 to B. burgdorferi flagellin specifically detects chaperonin-HSP60." ;
 RT Biochim. Biophys. Acta 1181:97-100 (1993).
 RC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR HSSP; P06139; 1AQN;
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding; Mitochondrion.
 FT NON-TER 22
 SQ SEQUENCE 22 AA; 2303 MW; E09D2EB934475F5 CRC64;

Query Match Score 20; DB 1; Length 22;
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;
 Matches 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ADHRQLQ 9
 Db 8 ADARALML 15

RESULT 12
 ID ODPB_BOVIN STANDARD; PRT; 24 AA.
 AC P11966;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT (EC 1.2.4.1) (FRAGMENT).
 DE PDHB.
 OS Bos taurus (Bovine).
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Bovinae; Bos.
 OC NCBITaxonID=9913;
 RP SEQUENCE.
 RXN MEDLINE=88134251; PubMed=2829898;
 RA Ho L., Javed A.A., Pepin R.A., Thekkumkara T.J., Raefsky C., Nole J.B., Caliendo A.M., Kwon M.S., Kerr D.S., Patel M.S.;
 RA "Identification of a cDNA clone for the beta-subunit of the pyruvate dehydrogenase component of human pyruvate dehydrogenase complex." ;
 RT Biochem. Biophys. Res. Commun. 150:904-908 (1988).
 RI -1- FUNCTION: THE PYRUVATE DEHYDROGENASE COMPLEX CATALYZES THE OVERALL

CONVERSION OF PYRUVATE TO ACETYL-COA & CO(2). IT CONTAINS MULTIPLE COPIES OF THREE ENZYMATIC COMPONENTS: PYRUVATE DEHYDROGENASE (E1), DIHYDROLIPOAMIDE ACETYLTRANSFERASE (E2) & LIPOAMIDE DEHYDROGENASE (E3).
 CC -1- CATALYTIC ACTIVITY: PYRUVATE + LIPOAMIDE = S-ACETYL-DIHYDRO-LIPOAMIDE + CO(2).
 CC -1- COFACTOR: THIAMINE PYROPHOSPHATE.
 CC -1- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 DR PIR; B27712; B27712.
 KW Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate; Mitochondrion.
 FT NON-TER 24
 SQ SEQUENCE 24 AA; 2849 MW; 0E9DF43248221854 CRC64;

Query Match Score 20; DB 1; Length 24;
 Best Local Similarity 27.3%; Pred. No. 1.7e+03;
 Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 7 LOQISSLQQ 17
 Db 1 LOVTVREAINQ 11

RESULT 13
 ID RECJ_SALTY STANDARD; PRT; 14 AA.
 AC P28355;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1.1.-) (FRAGMENT).
 GN RECJ.
 OS Salmonella typhimurium
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91046011; PubMed=2236050;
 RA Kawakami K., Nakamura Y.;
 RT "Autogenous suppression of an opal mutation in the gene encoding peptide chain release factor 2." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8432-8436 (1990).
 CC -1- FUNCTION: SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE. REQUIRED FOR MANY TYPES OF RECOMBINATIONAL EVENTS, ALTHOUGH THE STRINGENCY OF THE REQUIREMENT FOR RECJ APPEARS TO VARY WITH THE TYPE OF RECOMBINATIONAL EVENT MONITORED AND THE OTHER RECOMBINATION GENE PRODUCTS WHICH ARE AVAILABLE.
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 CC -----
 CC DR EMBL; M38590; AAA72913.; -.
 DR StcGene; SG10332; recJ.
 KW Hydrolase; Nuclease; Exonuclease.
 FT NON-TER 1
 SQ SEQUENCE 14 AA; 1696 MW; 105E784AC26C5650 CRC64;

Query Match Score 19; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HRQLQLSI 11
 Db 1 NRSLQIII 8

RESULT 14
TPIS_PINPS STANDARD; PRT; 17 AA.
ID
AC P81666;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (EC 5.3.1.1) ("TIM") (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN
RP
SEQUENCE.
RC TISSUE_Needle;
RX MEDLINE-9924088; PubMed-10344291;
RA Costa P., Pilonneau C., Bauw G., Dubois C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -|- CATALYTIC ACTIVITY: D-GLUCERALDEHYDE 3 PHOSPHATE = DIHYDROXY-
 ACETONE PHOSPHATE.
CC -|- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -|- INDUCTION: BY WATER STRESS.
CC -|- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
 AND PLASTID.
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N139) IS: 5.9, ITS MW IS: 24 kDa.
CC -|- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR InterPro; IPR000652;
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt; Multigene family.
FT NON_TER 1
FT NON_CONS 9 10
FT NON_TER 17 17
FT SEQUENCE 17 AA; 2053 MW; 183DB41757AF13CB CRC64;
Query Match
Best Local Similarity 21.6%; **Score** 19; **DB** 1; **Length** 18;
Matches 3; **Conservative** 3; **Mismatches** 1; **Indels** 0; **Gaps** 0;
Qy 14 CLQQL 18
Db 5 CYEQL 9
RESULT 15
FIXA_RHILE STANDARD; PRT; 18 AA.
ID
AC P14313;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE FIXA PROTEIN (FRAGMENT).
GN FIXA.
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=384;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9006358; PubMed-2555670;
RA Hontelez J.G.J., Lankhorst R.K., Katinakis P., van den Bos R.C.,
RA van Rammen A.;
RT Characterisation and nucleotide sequence of a novel gene fixW
RT upstream of the fixABC operon in Rhizobium leguminosarum.";

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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:16:04 ; Search time 114.89 Seconds
(without alignments)
18.363 Million cell updates/sec

Title: US-09-165-546A-8
Perfect score: 88
Sequence: 1 AADHRQLSISSSCLQQL 18

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_15:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rhodent:
 12: sp_unclassified:
 13: sp_vertebrate:
 14: sp_virus:
 15: sp_yeast:
 16: sp_zebrafish:
 17: sp_chicken:
 18: sp_dog:
 19: sp_cat:
 20: sp_horse:
 21: sp_chimpanzee:
 22: sp_gorilla:
 23: sp_baboon:
 24: sp_rhesus:
 25: sp_macaque:
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 32: sp_chaffinch:
 33: sp_bird:
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 35: sp_worm:
 36: sp_mosquito:
 37: sp_drosophila:
 38: sp_cabbage:
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 893: sp_mackerel:
 894: sp_bluefin:
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 896: sp_mackerel:
 897: sp

OC	Erwinia		OS	Artemia salina (Brine shrimp)	
OX	NCBI_TAXID=557;		OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;	
RN	[1]		OC	Artemidiidae; Artemia.	
RP	SEQUENCE FROM N.A. PubMed=9422601;		OX	NCBI_TAXID=85549;	
RX	MEDLINE=98083064; Subramanian P.S., Xie G., Xia T., Jensen R.A.; "Substrate ambiguity of 3-deoxy-D-manno-octulosonate 8-phosphatase synthase from <i>Neisseria gonorrhoeae</i> in the context of its membership in a protein family containing a subset of 3-deoxy-D-arabinohexitulosonate 7-phosphate synthases."; J. Bacteriol. 180:119-127 (1998).		RN	SEQUENCE FROM N.A. [1]	
RT	EMBL: U93355; AAB6401.1; -.		RX	NCBI_TAXID=93321609; PubMed=8101168;	
RT	Hypothetical protein.		RA	Shenk M.A., Bode H.R., Steele R.E.; "Expression of <i>Cnox-2</i> , a HOM/HOX homeobox gene in hydra, is correlated with axial pattern formation."; Development 117:657-667 (1993).	
RT	NON_TER 1 1		RL	EMBL: M62873; AAC83403.1; -.	
FT	SEQUENCE 24 AA; 2725 MW; 34989DD773855CEE CRC64;		DR	HSSP; P02833; IHOM.	
SQ	Query Match 29.5%; Score 26, DB 2; Length 24; Best Local Similarity 38.1%; Pred. No 7.2e+02; Matches 8; Conservative 4; Mismatches 1; Indels 8; Gaps 1;		DR	INTERPRO; IPR001356;	
			DR	Pfam; PF00046; homeobox; 1.	
			DR	KW Homeobox; DNA-binding; Nuclear protein.	
			FT	PFAM; PF00046; homeobox; 1.	
			FT	RNMebox; DNA-binding; Nuclear protein.	
			FT	RT	
			FT	NON_TER 25 25	
			FT	NON_TER 25 25	
			SQ	SEQUENCE 25 AA; 3127 MW; 1AB483ADC8A3BFDCF CRC64;	
			QY	5 ROLQLSISCLQQ 17	
			DB	9 RRIEWAHSCLITE 21	
			RESULT	5	
			ID	Q9PWR9 PRELIMINARY; PRT; 25 AA.	
			AC	DT 01-MAY-2000 (TREMBLrel. 13, Created)	
			DT	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
			DT	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
			DE	DE MELANOMA RECEPTOR TYROSINE KINASE (FRAGMENT).	
			OS	OS <i>Xiphophorus maculatus</i> (Southern platyfish).	
			OC	OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha; Poeciliidae; <i>Xiphophorus</i> .	
			OC	NCBI_TAXID=8083;	
			RN	RN [1]	
			RP	SEQUENCE FROM N.A.	
			RC	STRAIN=ONC SR-STRAIN;	
			RA	RA Schartl M., Wilde B.; Hornung U.;	
			RT	RT "triplet repeat variability in the signal peptide sequence of the Xmrk receptor tyrosine kinase gene in <i>Xiphophorus fish</i> .";	
			RL	RL Gene 224:17-21(1998).	
			DR	DR EMBL; U82804; ADD10123.1; -.	
			KW	KW Receptor; Kinase.	
			FT	FT NON_TER 25 25	
			SQ	SEQUENCE 25 AA; 2695 MW; 967AF74362DF4350 CRC64;	
			QY	7 IQLSSSC 14	
			DB	15 LVLSISRC 22	
			RESULT	6	
			ID	Q9S919 PRELIMINARY; PRT; 17 AA.	
			AC	DT 01-MAY-2000 (TREMBLrel. 13, Created)	
			DT	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
			DT	DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)	
			DE	DE ANTENNAFEDIA CLASS HOMEBOX RELATED PROTEIN (FRAGMENT).	
			GN	GN CNHV4.	

OS Herdmania momus.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Asciidaeae.
 OC Stolidobranchia; Pyuriidae; Herdmania.
 OX NCBI_TAXID=7733;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE=EMBRYO;
 RA Bennett C.V.D.;
 Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U09802; AAA8627.1; -.
 DR HSSP; P02833; 1HOM;
 INTERPRO; IPR001356;
 PFAM; PF00044; homeobox; 1.
 KW Homeobox; DNA-binding; Nuclear protein.
 FT NON_TER 1
 FT NON_TER 21
 SQ SEQUENCE 21 AA; 21 MW; 5DCDB3BF1556500C CRC64;

Query Match 11
 Best Local Similarity 23.18%; Score 24; DB 5; Length 21;
 Matches 3; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 QY 5 RQLQSISSC1QQ 17
 Db 8 RRIETAHALCLSE 20

RESULT 11
 Q91103 PRELIMINARY; PRT; 22 AA.
 ID Q91103
 AC Q91103
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HOXA4-LIKE HOMEODOMAIN PROTEIN (FRAGMENT).
 OS Morone saxatilis (Striped bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleoste; Neoteleoste;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Percoidae;
 OC Moronidae; Morone.
 OX NCBI_TAXID=34816;

RN [1]
 SEQUENCE FROM N.A.
 TISSUE=BLOOD;
 MEDLINE=95005122; PubMed=7921046;
 RA Pavel A.M., Stellwag E.J.;
 RT "Survey of Hox-like genes in the teleost Morone saxatilis:
 implications for evolution of the Hox gene family.";
 RL Mol. Mar. Biol. Biotechnol. 3:149-157(1994).
 DR EMBL; U09945; AAC59651.1; -.
 DR HSSP; P02833; 1HOM;
 INTERPRO; IPR001356; -.
 DR PFAM; PF00044; homeobox; 1.
 KW Homeobox; Nuclear protein; DNA-binding.

FT NON_TER 22
 SQ SEQUENCE 22 AA; 2733 MW; 37594B33CDB3D/B4 CRC64;

Query Match 12
 Best Local Similarity 23.18%; Score 24; DB 13; Length 22;
 Matches 3; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 QY 5 RQLQSISSC1QQ 17
 Db 6 RRIETAHALCLSE 18

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HOXA5-LIKE HOMEODOMAIN PROTEIN (FRAGMENT).
 OS Morone saxatilis (Striped bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleoste; Neoteleoste;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Moronidae; Morone.
 OX NCBI_TAXID=34816;
 RN [1]
 SEQUENCE FROM N.A.
 TISSUE=BLOOD;
 MEDLINE=95005122; PubMed=7921046;
 RA Pavel A.M., Stellwag E.J.;
 RT "Survey of Hox-like genes in the teleost Morone saxatilis:
 implications for evolution of the Hox gene family.";
 RL Mol. Mar. Biol. Biotechnol. 3:149-157(1994).
 DR EMBL; U09949; AAC59655.1; -.
 DR INTERPRO; IPR001356; -.
 DR PFAM; PF00044; homeobox; 1.
 KW Homeobox; Nuclear protein; DNA-binding.
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2726 MW; 37494DADCDDB3D/B4 CRC64;

Query Match 13
 Best Local Similarity 23.18%; Score 24; DB 13; Length 22;
 Matches 3; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 QY 5 RQLQSISSC1QQ 17
 Db 6 RRIETAHALCLSE 18

Db 6 RRIEIAHALCLSE 18

RESULT 14

ID Q25139 PRELIMINARY; PRT; 23 AA.

AC Q25139.01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HROXB (FRAGMENT).

GN HROXB.

OS *Haliothis rufescens* (California red abalone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;

OC Halitidae; Haliotis.

OX NCBI_TaxID=6454;

RN [1]

RP SEQUENCE FROM N.A.

RA Degnan B.M.;

RL Submitted (MAY-1994) to the EMBL/GenBank/DDJB databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93372986; PubMed=7689904;

RA Degnan B.M.; Morse D.E.;

RT "Identification of eight homeobox-containing transcripts expressed during larval development and at metamorphosis in the gastropod mollusc *Haliothis rufescens*."

RT Mol. Mar. Biol. Biotechnol. 2:1-9(1993).

RL EMBL; X79377; CNA55922.1; -

DR HSSP; P02833; IHOM.

DR INTERPRO; IPR001356; -

DR PFAM; PF00046; homeobox; 1.

FT NON_TER 1 23 23

FT NON_TER 1 23 23

SQ SEQUENCE 23 AA; 2872 MW; FFADCDB3BF153F4A CRC64;

Query Match 27.3%; Score 24; DB 5; Length 23;

Best Local Similarity 23.1%; Pred. No. 1.6e+03;

Matches 3; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 5 RQLQTSSSLQQ 17

Db 9 RRIEIAHALCLSE 21

RESULT 15

ID Q23965 PRELIMINARY; PRT; 25 AA.

AC Q23965.01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HOMEO DOMAIN PROTEIN (FRAGMENT).

OS *Dendrocoelum lacteum*.

OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Tricladida;

OC Paludicola; Dendrocoeliidae; Dendrocoelium.

OX NCBI_TaxID=27835;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95565341; PubMed=7638172;

RA Balavoine G., Telford M.J.;

RT "Identification of planarian homeobox sequences indicates the antiquity of most Hox/homeotic gene subclasses.";

RL Proc. Natl. Acad. Sci. U.S.A. 92:7227-7231(1995);

EMBL; L41858; AAB17631.1; -

DR HSSP; P02833; IHOM.

DR INTERPRO; IPR001356; -

DR PFAM; PF00046; homeobox; 1.

KW Homeobox; DNA-binding; Nuclear protein.

FT NON_TER 1 25 25

FT NON_TER 1 25 25

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: May 8, 2001, 15:07:07 ; Search time 113.31 seconds

(without alignments)
9.081 Million cell updates/sec

Title: US-09-165-546A-9
Perfect score: 84

Sequence: 1 VILKEFTVSGNLTIRLT 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 5716325 residues

Total number of hits satisfying chosen parameters: 165078

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0401;*

1: /SIDS6/gcadata/geneseq/geneseq/AA1980.DAT;*

2: /SIDS6/gcadata/geneseq/geneseq/AA1981.DAT;*

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18: /SIDS6/gcadata/geneseq/geneseq/AA1997.DAT;*

19: /SIDS6/gcadata/geneseq/geneseq/AA1998.DAT;*

20: /SIDS6/gcadata/geneseq/geneseq/AA1999.DAT;*

21: /SIDS6/gcadata/geneseq/geneseq/AA2000.DAT;*

22: /SIDS6/gcadata/geneseq/geneseq/AA2001.DAT;*

ALIGNMENTS

RESULT 1
Y52436

ID Y52436 standard; Protein: 17 AA.

XX

AC Y52436;

XX

DT 15-FEB-2000 (first entry)

XX

DE Human tumour antigen NY-ESO-1 peptide #9.

XX

KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;

KW T-cell; helper; stimulation; proliferation; treatment;

KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;

KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;

KW lymphoma.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN W09953938-A1.

XX

PD 28-OCT-1999.

XX

PF 24-MAR-1999;

XX

99WO-US066875.

PR 17-APR-1998;

98US-0062422.

PR 02-OCT-1998;

98US-0165346.

XX

PA (LUDWIG INST CANCER RES.

XX

PI Stockert E, Jager E,

Chen Y, Scanlan M, Alexander K, Old LJ;

PI Gure A, Ritter G;

XX

DR WP1; 2000-038483/03.

SUMMARIES

% Query Match Length DB ID Description

Result No. Score

Score

Query

Match

Length

DB

ID

Description

Human tumour antigen

XX Novel peptides which bind to MHC class I and MHC class II molecules
PT useful for therapeutic and diagnostic purposes
PS Claim 4; Page 22; 49pp; English.
XX Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC (major
CC histocompatibility Class II HLA-DR53 molecules thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.

XX Sequence 17 AA;

Query Match 81.5%; Score 68.5%; DB 21; Length 17;
Best Local Similarity 94.4%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 1 vlkkeftvsgnilitrlt 18

Qy 1 VLKKEFTVSGNILITRLT 18
||| | | | | | | | | | | | | |
Db 1 vlkkeftvsgnilitrlt 17

RESULT 2
Y52440
ID Y52440 standard; Protein; 18 AA.

XX 15-FEB-2000 (first entry)
DE Human tumour antigen NY-ESO-1 peptide #13.
XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
KW T-cell; helper; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX Synthetici.
OS Homo sapiens.
XX WO9953938-A1.

XX 28-OCT-1999.
PF 24-MAR-1999; 99WO-US06875.

XX 17-APR-1998; 98US-0062422;
PR 02-OCT-1998; 98US-0165546.

XX (LUDW-) LUDWIG INST CANCER RES.
PF 24-MAR-1999; 99WO-US06875.

XX 17-APR-1998; 98US-0062422;
PR 02-OCT-1998; 98US-0165546.

XX DR WPI; 2000-038483/03.

XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX DR WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules
PT useful for therapeutic and diagnostic purposes

PS Claim 4; Page 22; 49pp; English.

XX Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human
CC tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC (major
CC histocompatibility Class II HLA-DR53 molecules thereby stimulating
CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
CC localisation studies revealed it to be expressed at high levels
CC in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included
CC melanoma specimens and cell lines, and breast and bladder cancer
CC specimens, with expression in other tumour types being sporadic.
CC These NY-ESO-1-derived peptides may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of
CC cancers (such as melanoma, breast cancer, prostate cancer, lung
CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC or lymphoma) and to stimulate the proliferation of T cells.

XX Sequence 18 AA;

Query Match 66.7%; Score 56; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TVSGNILITRLT 18
||| | | | | | | | | | | | |
Db 1 tvsgnilitrlt 12

RESULT 3
Y06001
ID Y06001 standard; Peptide; 10 AA.

XX

AC Y06001;

XX

DT 16-AUG-1999 (first entry)

XX

DB Human cancer antigen NY ESO-1/CAG-3 HLA Peptide motif.

XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;

KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;

KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;

KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;

KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;

KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;

KW vaccine; human leukocyte antigen; HLA.

XX

OS Homo sapiens.

XX

PN WO918206-A2.

XX

PD 15-APR-1999.

XX

PF 21-SEP-1998;

XX

PR 08-OCT-1997;

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Rosenberg SA, Wang RF;

XX

XX

DR WPI; 1999-277270/23.

XX

Cancer antigen NY ES01/CAG-3

XX

PS Example 10; Page 42; 88pp; English.

XX

CC This peptide was identified as an HLA peptide motif following a
CC screen for epitopes from the coding region of human NY ESO-1/CAG-3
CC ORF1 (see X58599). 30 Epitopes (see Y05988-Y06017) were identified.
CC The present peptide (ranked 14) corresponds to amino acid residues

126-135 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukemia, uterine adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

Sequence 10 AA;

Query Match Score 48; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0088; Indels 0;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;
Db 6 FTVSGNLTI 15
1 I|||||||
1 ftvsgnlti 10

RESULT 4
Y52437 standard: Protein; 19 AA.
ID Y52437;

AC Y52437;
XX DT-FEB-2000 (first entry)
XX Human tumour antigen NY-ESO-1 peptide #10.
DE Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
T-cell; helper; stimulation; proliferation; treatment;
diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.
XX Synthetic.
OS Homo sapiens.
PN WO9951938-A1.
XX PD 28-OCT-1999.
XX PF 24-MAR-1999; 99WO-US06875.
XX PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.
(LUDWIG) LUDWIG INST CANCER RES.
XX PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX DR 2000-038483/03.
XX WPI; 2000-038483/03.

Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC major histocompatibility Class II HLA-DR53 molecules, thereby stimulating proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and

tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.

Sequence 19 AA;

Query Match Score 48; DB 21; Length 19;

Best Local Similarity 83.3%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 1; Indels 0;
Gaps 0;

Qy 1 VLLKEFTYSQNI 12
ID Y05988 standard; Peptide; 10 AA.
XX Y05988;
AC Y05988;
XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.
XX OS Homo sapiens.
XX PN WO9918205-A2.
XX PD 15-APR-1999.
XX PF 21-SEP-1998; 98WO-US19609.
XX PR 08-OCT-1997; 97US-0051428.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rosenberg SA, Wang RF;
XX DR WPI; 1999-27270/23.
XX PT Cancer antigen NY ESO1/CAG-3
XX PS Example 10; Page 42; 80pp; English.

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y05988-Y06017) were identified. The present Peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer Peptides (see Y05967-87) derived from CAG-3 portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and

Novel Peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes

Claim 4: Page 22; 49pp; English.
Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human tumour antigen, NY-ESO-1 (Y52430) which can bind to MHC major histocompatibility Class II HLA-DR53 molecules, thereby stimulating proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and

CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX Sequence 10 AA;
 SQ Query Match 56.0%; Score 47; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 TVSGNLTIR 16
 Db 1 tvsgnltir 10

RESULT 6
 Y05980 standard; Peptide; 10 AA.
 ID Y05980
 XX
 AC Y05980;
 XX
 DT 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127.
 DE NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adeno carcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX Homo sapiens.
 OS
 PN W09918206-A2.
 PD 15-APR-1999.
 XX
 PF 21-SEP-1998; 98WO-US19609.
 PR 08-OCT-1997; 97US-0061428.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rosenberg SA, Wang RF;
 XX DR; WPI: 1999-277270/23.
 PT Cancer antigen NY ESO1/CAG-3
 XX
 PS Claim 17; Page 64; 88pp; English.
 This sequence represents cancer peptide ESO10-127 that corresponds
 CC to amino acid residues 127-136 of human ESO-1/CAG-3 (or cAG-3) ORF1
 CC (see Y09665). a new and potent tumour antigen capable of eliciting
 CC an antigen specific immune response by T cells. Cancer peptides
 CC derived from CAG-3 ORF1, CAG-3 ORF2 (see Y05966), portions of them
 CC and their variants (see Y05967-87), are useful as cancer vaccines
 CC that protect against cancer. The invention provides: vectors and
 CC host cells (also useful as vaccines); a method of diagnosis of
 CC cancer or precancer; a transgenic animal; antisense oligonucleotides
 CC that inhibit expression of the cancer peptide or tumour antigen;
 CC antibodies reacting with a CAG-3 cancer peptide, useful in
 CC diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without
 CC an HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers. Melanoma is treated by inducing cancer-specific T
 CC cells in vitro for subsequent return to a patient.

XX Sequence 10 AA;
 SQ Query Match 56.0%; Score 47; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 TVSGNLTIR 16
 Db 1 tvsgnltir 10

RESULT 7
 Y79753
 ID Y79753 standard; Peptide; 9 AA.
 XX
 AC Y79753;
 XX
 DT 10-MAY-2000 (first entry)
 XX
 DE NY-ESO-1 derived peptide #9.
 XX
 KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1;
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CTL;
 KW cytostatic; melanoma; synovial sarcoma.
 XX
 OS Homo sapiens.
 XX
 PN WO200000824 A1.
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14493.
 PR 26-JUN-1999; 98US-0105839.
 PA (LUDWIG INST CANCER RES.
 XX
 PI Turcic O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
 PI Chen Y, Gure A, Old LJ;
 XX
 DR WPI: 2000-170933/15.
 XX
 PT Determining the possible presence of breast, endometrial, colorectal,
 PT lung, bladder or head-neck cancer
 XX
 PS Example 13; Page 26; 40pp; English.
 XX
 CC A method has been developed for determining the possible presence of a
 CC cancer, which is not melanoma or synovial sarcoma. The method comprises
 CC assaying a sample taken from the subject to determine the expression of a
 CC SSX gene, and determining the expression as a determination of the
 CC possible presence of cancer. Expression of SSX1 gene indicates possible
 CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
 CC cancer. These cancers are also detected by SSX2 and SSX4 gene expression.
 CC SSX2 gene expression additionally indicates possible presence of
 CC lymphoma, renal cell cancer, glioma and prostate cancer. Expression of
 CC SSX4 gene also indicates possible presence of ovarian or stomach cancer.
 CC SSX5 gene expression indicates the same cancers as SSX1, except breast
 CC cancer. Determining expression of SSX gene can be used to monitor
 CC progress of melanoma or synovial sarcoma, which is not cancer. The
 CC SSX derived peptide complex stimulates proliferation of cytolytic T
 CC cells. This is useful for treating cancer, especially melanoma. Y79464
 CC to Y79468 represent specifically claimed HLA binding peptides for use in
 CC the method of the invention. Z88452 to Z88465 represent PCR primers used
 CC in the isolation of SSX genes in the exemplification of the present
 CC invention. Y78469 to Y78500, and Y79684 to Y79762 represent peptides
 CC derived from SSX proteins or NY-ESO-1, which are used in the
 CC exemplification of the present invention.
 XX Sequence 9 AA;
 SQ

KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;	OS Homo sapiens.
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;	XX XX
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;	PN WO9918206-A2.
KW liver cancer; sarcoma; tumour; immunotherapy; therapy;	PD 15-APR-1999.
KW vaccine; human leukocyte antigen; HLA.	XX
XX OS Homo sapiens.	XX
XX PN WO9918206-A2.	PD 15-APR-1999.
XX PD 15-APR-1999.	XX
XX PR 21-SEP-1998;	PF 21-SEP-1998;
XX PR 08-OCT-1997;	PR 08-OCT-1997;
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.	PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PR 08-OCT-1997;	PR 08-OCT-1997;
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.	PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rosenberg SA, Wang RF;	PI Rosenberg SA, Wang RF;
XX DR 1999-277270/23.	DR 1999-277270/23.
XX Cancer antigen NY ESO1/CAG-3	XX Cancer antigen NY ESO1/CAG-3
XX PS Example 10; Page 43; 88PP; English.	PS Example 10; Page 43; 88PP; English.
XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y06018-47) were identified. The present peptide (ranked 11) corresponds to amino acid residues 131-139 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.	XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y06018-47) were identified. The present peptide (ranked 11) corresponds to amino acid residues 131-139 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.
XX Sequence 9 AA;	XX Sequence 9 AA;
Query Match 44.0%; Score 37; DB 20; Length 9;	Query Match 44.0%; Score 37; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;	Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VLLKEFTV 8	Qy 1 VLLKEFTV 8
Db 2 vllkeftv 9	Db 1 nlltirlt 8
RESULT 13	RESULT 14
ID Y06028 standard; Peptide: 9 AA.	ID Y06000 standard; Peptide: 10 AA.
XX AC Y06028;	DB 1 nlltirlt 8
XX DT 16-AUG-1999 (first entry)	XX AC Y06000;
XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.	XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX KW ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;	XX KW ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; Hodgkin's lymphoma; lung cancer;
XX KW leukaemia; non-Hodgkin's lymphoma; adenocarcinoma; thymoma; colon cancer;	XX KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
XX KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;	XX KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
XX KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;	XX KW vaccine; human leukocyte antigen; HLA.
XX OS Homo sapiens.	XX OS Homo sapiens.
XX PN WO9918206-A2.	XX PN WO9918206-A2.
XX PD 15-APR-1999.	XX PD 15-APR-1999.

Result No.	Score	Query Match	Length	DB ID	Description
1	33	39.3	25	1 US-08-087-772A-8	Sequence 8, Appl
2	28	33.3	12	1 US-07-778-233B-13	Sequence 13, Appl
3	28	33.3	12	1 US-07-963-321-13	Sequence 13, Appl
4	28	33.3	12	1 US-08-290-641-13	Sequence 13, Appl
5	28	33.3	12	1 US-08-548-540-13	Sequence 13, Appl
6	28	33.3	12	1 US-08-973-225-92	Sequence 13, Appl
7	28	33.3	17	6 5185441-3	Patent No. 5185441
8	27	32.1	21	1 US-08-704-170-28	Sequence 28, Appl
9	27	32.1	21	5 PCT-US94-02631-28	Sequence 28, Appl
10	26	31.0	14	2 US-08-664-640-92	Sequence 92, Appl
11	26	31.0	14	3 US-08-973-225-92	Sequence 92, Appl
12	26	31.0	14	3 US-08-973-225-217	Sequence 217, App
13	26	31.0	14	4 US-09-244-298A-92	Sequence 92, Appl
14	26	31.0	18	2 US-08-702-105A-15	Sequence 15, Appl
15	26	31.0	18	3 US-08-702-110A-15	Sequence 15, Appl
16	25	29.8	9	4 US-09-258-754-253	Sequence 253, App
17	25	29.8	11	1 US-08-665-966-4	Sequence 4, Appl
18	25	29.8	11	3 US-09-041-780-4	Sequence 4, Appl
19	25	29.8	23	1 US-08-248-505-2	Sequence 2, Appl
20	25	29.8	24	1 US-08-118-270-89	Sequence 89, Appl
21	25	29.8	24	2 US-08-789-078-18	Sequence 18, Appl
22	25	29.8	24	2 US-08-752-633-18	Sequence 18, Appl
23	25	29.8	24	2 US-08-752-633-18	Sequence 18, Appl
24	25	29.8	24	2 US-08-552-633-19	Sequence 19, Appl
25	25	29.8	24	3 US-08-944-975-15	Sequence 15, Appl
26	25	29.8	24	5 PCT-US93-08528-89	Sequence 89, Appl
27	25	29.8	24	5 PCT-US95-04886-18	Sequence 18, Appl

Db 8 LLALATVGGNLLVIT 21

RESULT 2
US-07-778-233B-13
Sequence 13, Application US/07778233B
Patent No. 5,201,70
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
CULL, Millard G.
APPLICANT: Miller, Jeff F.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,321
FILING DATE: 1992/01/05
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/778,223
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-50-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 57 3 0.9
US-07-963-321-13

Query Match Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLKEFTVSG 10
| :||| 111
Db 3 LRREFKVSG 11

RESULT 4
US-08-290-641-13
Sequence 13, Application US/08290641
Patent No. 5,498530
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
CULL, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,641
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/963,321
FILING DATE: 15-OCT-1992
APPLICATION NUMBER: US/07/778,223

RESULT 3
US-07-963-321-13
Sequence 13, Application US/07963321
Patent No. 5,338665
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
CULL, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California

FILING DATE: 16-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 11509-50-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 CLONE: 57 3 0.9
 US-08-548-540-13

Query Match 33.3%; Score 28; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

Qy 2 LLKEFTVSG 10
 | :| |||||
 Db 3 LRREFKVSG 11

RESULT 6
 PCT-US96-09809-13
 Sequence 13, Application PC/TRUS9609809
 GENERAL INFORMATION:
 APPLICANT: Schatz, Peter J.
 APPLICANT: Cull, Millard G.
 APPLICANT: Miller, Jeff F.
 APPLICANT: Stemmer, Willem P.C.
 APPLICANT: Gates, Christian M.
 TITLE OF INVENTION: Peptide Library and Screening Method
 NUMBER OF SEQUENCES: 162

CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/09809
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/548,540
 FILING DATE: 16-OCT-1995
 APPLICATION NUMBER: US 08/290,641
 FILING DATE: 15-AUG-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,321
 FILING DATE: 15-OCT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 16528J-001240US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids

Query Match 33.3%; Score 28; DB 5; Length 12;
 Best Local Similarity 66.7%; Pred. No. 59;
 Matches 6; Conservative 1; Mismatches 2; Indels 0;
 Gaps 0;

Qy 2 LLKEFTVSG 10
 | :| |||||
 Db 3 LRREFKVSG 11

RESULT 5
 PCT-US96-09809-13
 Sequence 13, Application US/08548540
 Patent No. 573331
 GENERAL INFORMATION:
 APPLICANT: Schatz, Peter J.
 APPLICANT: Cull, Millard G.
 APPLICANT: Miller, Jeff F.
 APPLICANT: Stemmer, Willem P.C.
 APPLICANT: Gates, Christian M.
 TITLE OF INVENTION: Peptide Library and Screening Method
 NUMBER OF SEQUENCES: 162

CORRESPONDENCE ADDRESS:
 ADDRESSEE: William M. Smith
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/548,540
 FILING DATE: 16-OCT-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/290,641
 FILING DATE: 15-AUG-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/963,321
 FILING DATE: 15-OCT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 16528J-001240US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids

Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 2;
Indels 0; Gaps 0;

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-704-170-28

Query Match 32.1%; Score 27; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 7;
Indels 0; Gaps 0;

Qy 2 LLKEFTVSG 10
| :|| |||
Db 3 LRREFKVSG 11

RESULT 7
51B541-3

; PATENT NO. S185441
; APPLICANT: WALLNER, BARBARA P.; SESSIONS, CATHERINE
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE
; FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/237, 309
; FILING DATE: 26-AUG-1988
; SEQ ID NO: 3;
; LENGTH: 17
51B541-3

Query Match 33.3%; Score 28; DB 6; Length 17;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 4;
Indels 0; Gaps 0;

Qy 7 TVSGNLTIRLT 18
| :|||:
Db 5 TVSGSLTIVNL 16

RESULT 8
US-08-704-170-28
; Sequence 28, Application US/08704170
; Patent No. 5707616

; GENERAL INFORMATION:
; APPLICANT: Douvas, Angeline
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Takehana, Yoshi
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Ehresmann, Glenn
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Spitals, John P.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 29, 215
; FILING DATE: 11-MAR-1993
; REFERENCE/DOCKET NUMBER: 1920-331
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-02631-28

Query Match 32.1%; Score 27; DB 5; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 7;
Indels 0; Gaps 0;

Qy 2 LLKEFTVSGNLTIRLT 17
| :|| | | | :
Db 3 LRREFEVYGPPIKRIHM 18

RESULT 10
US-08-764-640-92
; Sequence 92, Application US/08764640
; Patent No. 5869451

Patent No. 5869451 5837683

GENERAL INFORMATION:

APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Cwirka, Steven E.
 APPLICANT: Gates, Christian
 APPLICANT: Schatz, Peter J.
 APPLICANT: Balasubramanian, Palaniappan
 APPLICANT: Wagstrom, Christopher R.
 APPLICANT: Hendren, Richard W.
 APPLICANT: Deprince, Randolph B.
 APPLICANT: Podduturi, Surekha
 APPLICANT: Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 ZIP: 27709

TITLE OF INVENTION: RECEPTOR

CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 244
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 ZIP: 27709

ATTORNEY/AGENT INFORMATION:

NAME: Hribiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 92:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/764,640
 FILING DATE: 11-DEC-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:

NAME: Hribiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK3281
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-764-640-92

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

APPLICANT: Dower, William J.
 Barrett, Ronald W.
 Cwirka, Steven E.
 Duffin, David J.
 Gates, Christian
 Haselden, Sherrell S.
 Schatz, Peter J.
 Wagstrom, Christopher R.
 Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

NUMBER OF SEQUENCES: 232
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Glaxo Wellcome
 STREET: Five Moore Drive, P.O. Box 13398
 CITY: Research Triangle Park
 STATE: NC
 ZIP: 27709

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

SOFTWARE: PatentIn Release #1.0, Version #1.30

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973,225A
 FILING DATE: 04-DEC-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hribiec, Robert T.
 REGISTRATION NUMBER: 36,392
 REFERENCE/DOCKET NUMBER: PK30650USW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-248-1000
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 92:
 US-08-973-225-92

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 12
 US-08-973-225-217
 Sequence 217 Application US/08973225A
 Patent No. 6083913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;
		Indels	0;
		Gaps	0;

RESULT 11
 US-08-973-225-92
 Sequence 92 Application US/08973225A
 Patent No. 6033913

Query	Match	Score	Length
Qy	3 LKEFVSG 10	31.0%	3
Db	3 LKEFLHSG 10	75.0%	2
		Best Local Similarity	14;
		Matches	6;
		Conservative	0;
		Mismatches	2;

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/973,225A
 FILING DATE: 04 Dec-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: PK3065USW
 INFORMATION FOR SEQ ID NO: 217:
 TELEPHONE: 919-248-1000
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 217:
 US-08-973-225-217:

Query Match 31.0%; Score 26; DB 3; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LKEFTVSG 10
 Db 3 LKEFLHSG 10

RESULT 13
 US-09-244-298A-92
 Sequence 92, Application US/09244298A
 Patent No. 6121238

GENERAL INFORMATION:
 APPLICANT: Dower, William J.
 APPLICANT: Barrett, Ronald W.
 APPLICANT: Cwirla, Steven E.
 APPLICANT: Gates, Christian
 APPLICANT: Schatz, Peter J.
 APPLICANT: Balasubramanian, Palanikappan
 APPLICANT: Wagstrom, Christopher R.
 APPLICANT: Hendren, Richard W.
 APPLICANT: Deprince, Randolph B.
 APPLICANT: Podduturi, Surekha
 APPLICANT: Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
 RECEPTOR
 NUMBER OF SEQUENCES: 244

RESPONSIBILITY ADDRESS:
 STREET: Glaxo Wellcome
 CITY: Five Moore Drive, P.O. Box 13398
 STATE: NC
 COUNTRY: USA
 ZIP: 27709

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,298A
 FILING DATE: 11 DEC-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Hrubiec, Robert T.
 REGISTRATION NUMBER: 36,392

TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: PK3281
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids

TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-244-298A-92

Query Match 31.0%; Score 26; DB 4; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LKEFTVSG 10
 Db 3 LKEFLHSG 10

RESULT 14
 US-08-702-105A-15
 Sequence 15, Application US/08702105A
 Patent No. 5908839

GENERAL INFORMATION:
 APPLICANT: Levitt, Roy C.
 APPLICANT: Maloy, W. Lee
 APPLICANT: Kari, U. Prasad
 APPLICANT: Nicolaides, Nicholas C.

TITLE OF INVENTION: Asthma Associated Factors As Targets For Treating Atopic Allergies Including Asthma And Related Disorders
 TITLE OF INVENTION: Treating Atopic Allergies Including Asthma And Related Disorders
 NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner L.L.P.
 STREET: 1300 I Street N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,105A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/874,503
 FILING DATE: 13-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Fordis, Jean B.
 REGISTRATION NUMBER: 32384
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4400
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-702-105A-15

Query Match 31.0%; Score 26; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TVSGNLT 14
 Db 7 TAGNALT 14

RESULT 15
US-08-702-110A-15
Sequence 15, Application US/08702110A
Patent No. 6037149

GENERAL INFORMATION:

APPLICANT: Levitt, Roy C.
APPLICANT: Maloy, W Lee
APPLICANT: Kari, U. Prasad
APPLICANT: Nicolaides, Nicholas C.

TITLE OF INVENTION: Asthma Associated Factors As Targets For Treating Atopic Allergies Including Asthma And Related Disorders

TITLE OF INVENTION: Disorders

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner L.L.P.
ADDRESSSEE: 1300 I Street N.W., Suite 700
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,110A
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/874,503
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32984
REFERENCE/DOCKET NUMBER: 05387.0056-01000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-0000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-702-110A-15

Query Match 31.0%; Score 26; DB 3; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TWSGNILT 14
Db 7 TTAGNALT 14

Search completed: May 8, 2001, 15:05:12
Job time: 108 sec

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: May 8, 2001, 15:08:19 ; Search time 68.24 Seconds
 (without alignments)
 18.127 Million cell updates/sec

Title: US-09-165-546A-9

Perfect score: 84

Sequence: 1 VLLKEFTVSGNLTIRLT 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 6872935 residues

Total number of hits satisfying chosen parameters: 4929

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_67;*: 1: pir1;*: 2: pir2;*: 3: pir3;*: 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	39.3	20	2 S45637	oxido-reductase - P
2	29	34.5	12	2 PN0170	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
3	28	33.3	21	2 S58431	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
4	26	31.0	17	4 176673	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
5	26	31.0	19	2 S74114	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
6	25	29.8	11	2 165231	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
7	25	29.8	20	2 S57286	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
8	25	29.8	22	2 P00697	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
9	25	29.8	23	2 T4418	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
10	25	29.8	24	2 A24417	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
11	24	29.2	15	2 146909	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
12	24	28.6	20	2 S29817	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
13	24	28.6	22	2 B60771	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
14	24	28.6	24	2 S38729	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
15	23	28.0	22	2 C26627	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
16	23	27.4	10	2 PN0165	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
17	23	27.4	16	2 S36876	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
18	23	27.4	16	2 S69361	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
19	23	27.4	17	2 S8129	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
20	23	27.4	19	2 A47689	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
21	23	27.4	20	2 PL0039	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
22	23	27.4	21	2 S47200	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
23	23	27.4	21	2 S47197	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
24	23	27.4	22	2 S47199	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
25	23	27.4	24	2 S23121	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
26	23	27.4	25	2 D47689	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
27	22	26.2	12	2 S17540	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
28	22	26.2	15	2 PA0097	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)
29	22	26.2	19	2 S34459	alcohol dehydrogenase (EC 1.1.1.1) - fungus (<i>Fusarium sporotrichioides</i>) (fragment)

ALIGNMENTS

Qy	9 SGNLITRUT 18	39.38%; Pred. No. 26;	Score 33; DB 2;	Length 20;
Db	6 TGNLRLNLT 15	Mismatches 7; Conservative	1; Mismatches 2; Indels 0; Gaps 0;	

RESULT 1

S45637 oxido-reductase - *Proteus vulgaris* (fragment)

C: Species: *Proteus vulgaris*
 C: Date: 10-Dec-1994 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

R.Trautwein, T.; Krauss, F.; Lottspeich, F.; Simon, H.
 Eur. J. Biochem. 222, 1025-1032, 1994

A: Title: The (2R)-hydroxycarboxylate-viologen-oxidoreductase from *Proteus vulgaris* is a membrane protein.

A: Reference number: S45637; MUID:94298804

A: Accession: S45637

A: Status: preliminary

A: Molecule type: protein

A: Residues: 1-20 <TRA>

Query Match 39.38%;
 Best Local Similarity 70.0%;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 2

PN0170 alcohol dehydrogenase (EC 1.1.1.1) - fungus (*Fusarium sporotrichioides*) (fragment)

C: Species: *Fusarium sporotrichioides*
 C: Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 31-Jan-1997

R.Fukaya, N.; Chow, L.P.; Tsugiura, Y.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994

A: Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides* protein.

A: Reference number: PN0160

A: Accession: PN0170

A: Molecule type: protein

A: Residues: 1-12 <PUK>

C: Experimental source: strain M-1-1

C: Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 34.5%;
 Best Local Similarity 66.7%;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LIKEFTVSG 10

Db 2 LLKGTVBG 10

RESULT 3

S58431 phosphatidylinositol transfer protein isoform, 36K - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Accession: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-May-2000
 R;de Vries, K.J.; Heinrichs, A.A.J.; Cunningham, E.; Brunink, F.; Westerman, J.; Somerha
 Biochem. J. 310, 643-649, 1995
 A;Title: An isoform of the phosphatidylinositol-transfer protein transfers sphingomyelin
 A;Reference number: S58430; MUID:95382786
 A;Accession: 558431
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1 21 <DEV>
 C;Superfamily: human phosphatidylinositol transfer protein

Query Match Score 28; DB 2; Length 21;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLIKETFY 8
 Db 1 VLKEFVRY 8

RESULT 4

I76673 hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)
 N;Alternate names: COII/ND5 protein
 C;Species: mitochondrial Mus musculus (house mouse)
 C;Accession: 12-Aug-1996 #sequence_revision 16-Jul-1998 #text_change 20-Apr-2000
 C;Accession: I76673; I76674
 R;Nelson, I.; Gerssimov, S.; Marsac, C.; Lestienne, P.; Bourso, P.
 Mamm. Genome 4, 680-683, 1993
 A;Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic mice
 A;Reference number: I57011; MUID:94100239
 A;Accession: I76673
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1 17 <NEL1>
 A;Cross-references: GB:S68119; NID:9544777
 A;Accession: 176674
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 8-17 <NEL2>
 A;Cross-references: GB:S68119; NID:9544777
 C;Comment: This is the hypothetical translation of a sequence believed to result from a
 C;Genetics:
 A;Gene: COII/ND5
 A;Genetic code: SGC1
 C;Keywords: fusion protein; mitochondrion
 F;1-17/Region: cytochrome-c oxidase chain II
 F;8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match Score 26; DB 4; Length 17;
 Best Local Similarity 45.5%; Pred. No. 3.5e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 LKEFTVSGNL 13
 Db 5 LKPFITNNNNI 15

RESULT 5

S74114 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 R;Dieuaide-Noubhani, M.; Novikov, D.; Baumgart, E.; Vanhooren, J.C.T.; Fransen, M.; Goet
 Eur. J. Biochem. 240, 660-666, 1996

Query Match Score 25; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 6.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VLLKEFTVSG 10
 Db 5 VVLKVFPVVG 14

RESULT 8
 P00697 hemagglutinin [Imported] - rice (fragment)
 C;Species: Oryza Sativa (rice)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C;Accession: P00697
 R.; Komatsu, S.; Kaijwari, H.; Hirano, H.
 Theor. Appl. Genet. 86, 935-942, 1993
 A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
 A;Reference number: P00696
 A;Accession: PQ0697
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-22 <VLA>

Query Match 29.8%; Score 25; DB 2; Length 24;
 Best Local Similarity 38.5%; Pred. No. 7.4e+02;
 Matches 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VILLEKFTVSGNIL 13
 Db 12 VLLDNFTFPENLM 24

RESULT 11
 I46909 voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kda 1
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C;Accession: I46909
 R.; Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.
 Neuron 8, 899-905, 1992
 A;Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.
 A;Reference number: I46909; MUID:92265303
 A;Accession: I46909
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-15 <VNL>
 A;Cross-references: GB:S316895; NID:9249481; PIDN:AAB22180.1; PID:9249482

Query Match 29.8%; Score 25; DB 2; Length 15;
 Best Local Similarity 41.2%; Pred. No. 5.4e+02;
 Matches 7; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VILLEKFTVSGNLTIRL 17
 Db 2 VLLSLFTI--IIFTLEM 15

RESULT 12
 S29817 cytochrome P450 2C23 - rat (fragment)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 05-Mar-1999
 C;Accession: S29817
 R.; Marie, S.; Rousset, F.; Cresteil, T.
 Biochim. Biophys. Acta 1172, 124-130, 1993
 A;Title: Age- and tissue-dependent expression of CYP2C23 in the rat.
 A;Reference number: S29817; MUID:91176794
 A;Accession: S29817
 A;Molecule type: mRNA
 A;Residues: 1-20 <MAR>
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
 C;Keywords: heme; transmembrane protein

Query Match 29.2%; Score 24; DB 2; Length 15;
 Best Local Similarity 41.2%; Pred. No. 5.4e+02;
 Matches 7; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VILLEKFTVSGNLTIRL 17
 Db 2 VLLSLFTI--IIFTLEM 15

RESULT 13
 B60711 CD40 antigen Hu549 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
 C;Accession: B60711
 R.; Braeschi-Andersen, S.; Paulie, S.; Koho, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A;Title: Biochemical characteristics and partial amino acid sequence of the receptor
 A;Reference number: A60711; MUID:89093941
 A;Accession: B60711

Query Match 28.6%; Score 24; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 9e+02;
 Matches 3; Mismatches 3; Indels 0; Gaps 0;

Qy 8 VSGNLTIRL 17
 Db 7 IIGNLELN 16

RESULT 10
 A24417 interphotoreceptor retinoid-binding protein - sheep (fragment)
 N;Alternate names: interstitial retinol-binding protein
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
 C;Accession: A24417
 R.; Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A;Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
 A;Reference number: A91365; MUID:86301171
 A;Accession: A24417
 A;Molecule type: protein
 A;Residues: 1-24 <FON>
 C;Superfamily: interphotoreceptor retinoid-binding protein
 C;Keywords: duplication

A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-22 <BRA>
 C; Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match Score 24; DB 2; Length 22;
 Best Local Similarity 25.0%; Pred. No. 1e+03;
 Matches 3; Conservative 5; Mismatches 4; Indels 0;
 Gaps 0;

Qy 4 KEFTVSGNLTI 15
 | : : | : |
 Db 9 KQYLINGQCCTL 20

RESULT 14

S3B29 probable malate carrier - Lactococcus lactis (fragment)

C; Species: Lactococcus lactis
 C; Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
 C; Accession: S38729
 R; Ansaney, V.; Deguin, S.; Blondin, B.; Barre, P.
 FEBS Lett. 332, 74-80, 1993

A; Title: Cloning, sequencing and expression of the gene encoding the malolactic enzyme from
 A; Reference number: S38728; MUID: 54009693
 A; Accession: S38729
 A; Status: not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-24 <ANS>
 A; Experimental source: strain IL441
 C; Genetics:
 A; Gene: mleP
 C; Function:
 A; Description: catalyzes membrane potential generation via malate/lactate exchange

Query Match Score 24; DB 2; Length 24;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LKEFTVSG 10
 ||| : |
 Db 4 LKEFKISG 11

RESULT 15

C26627 apolipoprotein C-I - crab-eating macaque (fragment)

C; Species: Macaca fascicularis (crab-eating macaque)
 C; Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 31-Dec-1993
 C; Accession: C26627
 R; Herbert, P.N.; Bausserman, L.L.; Lynch, K.M.; Saritelli, A.L.; Kantor, M.A.; Nicolosi, J.; Biochemistry 26, 1457-1463, 1987
 A; Title: Homologues of the human C and A apolipoproteins in the Macaca fascicularis (cynomolgus monkey) genome
 A; Reference number: A26627; MUID: 87185451
 A; Accession: C26627
 A; Molecule type: protein
 A; Residues: 1-22 <HER>
 C; Superfamily: apolipoprotein A-I
 C; Keywords: lipid binding; lipoprotein; VLDL

Query Match Score 23.5; DB 2; Length 22;
 Best Local Similarity 63.6%; Pred. No. 1.2e+03;
 Matches 7; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 3 LKEFTVSGNIL 13
 |||| |
 Db 11 LKEF---GNTL 18

34	19	22.6	17	1	NU4M_TRIU	Q3684 trichophyto
35	19	22.6	19	1	FIBA_MUNMU	P14457 mutiarius m
36	19	22.6	20	1	ARO_AMMME	P46380 amycolatops
37	19	22.6	20	1	FRE3_LTIN	P56249 litoria inf
38	19	22.6	20	1	V890_BORPE	P81549 bordetella
39	19	22.6	21	1	EPA8_HUMAN	P2892 homo sapien
40	19	22.6	22	1	HST1_LLETTA	P55338 leishmania
41	19	22.6	23	1	NEU1_LTICE	P81872 litoria cae
42	19	22.6	24	1	CT31_LLTCI	P81851 litoria cit
43	19	22.6	24	1	LPTN_ECOLI	P09408 escherichia
44	19	22.6	25	1	IRBP_PIG	P12662 sus scrofa
45	19	22.6	25	1	YCX8_ODO61	P49834 Odontella s
ALIGNMENTS						
RESULT	1					
DHAG_COMTE		STANDARD;				
ID P80105;		PRT;				
AC		24 AA.				
DT 01-OCT-1996	(Rel. 34,	Created)				
DT 01-OCT-1996	(Rel. 34,	Last sequence update)				
DT 15-DEC-1998	(Rel. 37,	Last annotation update)				
DE ALDHYDE DEHYDROGENASE, GAMMA CHAIN (EC 1.2.99.3) (ALDH) (FRAGMENT).						
OS Comamonas testosteroni (Pseudomonas testosteroni).						
OC Bacteriia; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.						
OX NCBI_TaxID=285;						
RN [1]						
RP						
SEQUENCE.						
RC STRAIN=ATCC 15667;						
RA Luykx D.M.A.M., Kim S.W., de Vries S., Duine J.A.;						
RL Submitted (JUL '1996) to the SWISS-PROT data bank.						
CC -!- CATALYTIC ACTIVITY: AN ALDEHYDE + ACCEPTOR + H(2)O = AN ACID +						
CC REDUCED ACCEPTOR.						
CC -!- COFACTOR: MOLYBDENUM.						
CC -!- SUBUNIT: HETEROTRIMERIC COMPOSED OF AN ALPHA, A BETA AND A GAMMA CHAIN.						
CC OXIDOREDUCTASE; Molybdenum.						
FT NON_TER	24	24				
SEQUENCE	24 AA:	2585 MW:	9E66B518130EA938 CRC64;			
Query Match	32.1%	Score 27;	DB 1;	Length 24;		
Best Local Similarity	45.5%	pred. No. 1.4e+02;				
Matches	5;	Mismatches	3;	Indels	0;	Gaps 0
CC CHAIN.						
CC OXIDOREDUCTASE; Molybdenum.						
KW LEU9.						
FT NON_TER	24	24				
SQ SEQUENCE	24 AA:	2585 MW:	9E66B518130EA938 CRC64;			
Qy 5 EFTVSGNILETI 15	:	111:1	:			
Db 4 QFTVNGRAASI 14						
RESULT	2					
LPL_CORG1		STANDARD;				
ID P42456;		PRT;				
AC		22 AA.				
DT 01-NOV-1995	(Rel. 32,	Created)				
DT 01-NOV-1995	(Rel. 32,	Last sequence update)				
DT 01-OCT-1996	(Rel. 34,	Last annotation update)				
DE LEU9 LEADER PEPTIDE.						
GN LEU9.						
OS Corynebacterium glutamicum (Brevibacterium flavum).						
OC Bacteriia; Firmicutes; Actinobacteria; Actinomycetales; Corynebacteriidae;						
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;						
OC Corynebacterium.						
OX NCBI_TaxID=1718;						
RN [1]						
RP						
SEQUENCE FROM N.A.						
RC STRAIN=ATCC 1.3032;						
RX MEDLINE=9416495; PubMed=8117072;						
RA Patek M., Krumbach K., Eggeling L., Sahm H.;						
RT "Leucine synthesis in Corynebacterium glutamicum: enzymatic activities, structure of leu9, and effect of leu9 inactivation".						

RT synthesis.";	
APPL Environ. Microbiol. 60:133-140(1994).	
-I FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS OF LEUCINE (BY SIMILARITY).	
CC	
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CC	
DR EMBL: X70959; CAA50295_1; ALT_TERML.	
KW Leader Peptide; Leucine biosynthesis.	
SEQUENCE 22 AA; 2535 MW; BB6E3DA8604AD7F8 CRC64;	
QY	2 LLKEFTVSGNLTIR 16
Db	:1:-1 :1:-1 1 MLHHMTSRLNLLR 15
RESULT 3	
ID TRBP_SHEEP STANDARD; PRT; 24 AA.	
AC P12665;	
RP SEQUENCE. MEDLINE=86301171; PubMed=3743780;	
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,	
RB Bridges C.D.B.;	
RT "N-terminal sequence homologies in interstitial retinol-binding proteins from 10 vertebrate species.";	
RL FEBS Lett. 205:309-312(1986).	
-I FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.	
CC SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT EPITHELIUM CELLS.	
CC PIR: A24417; A24417.	
KW Vitamin A; transport.	
NON_TER FT SEQUENCE 24 AA; 2799 MW; 02EDEBE61A8E4523 CRC64;	
QY 1 VLLKEFTVSGNLTIR 13	
Db 12 VLDDNTFPENIL 24	
RESULT 4	
CC4_CHIOP STANDARD; PRT; 20 AA.	
AC P341556;	
RP SEQUENCE. TISSUE=Hepatopancreas; MEDLINE=92120073; PubMed=1663026;	
RA Klimova O.A., Vedishcheva Y.V., Strongin A.Y.;	
RB "Isolation and characteristics of collagenolytic enzymes from the hepatopancreas of the crab Chionoecetes opilio.";	
RT DOI: Akad. Nauk SSSR 317:482-484(1991).	
-I FUNCTION: THIS ENZYME IS A METAL PROTEASE CAPABLE OF DEGRADING THE NATIVE TRIPLE HELIX OF COLLAGEN.	
CC -1 COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).	
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A (ZINC METALLOPROTEASE); ALSO KNOWN AS THE ASTACIN SUBFAMILY.	
CC HSSP: P07584; 1.IAD.	
DR MEROPS: M12.001;	
DR InterPro: IPRO00130; -.	
DR PROSITE: PS00142; ZINC_PROTEASE; PARTIAL.	
KW Hydrolase; Metalloprotease; Zinc; Collagen degradation.	
FT NON_TER FT SEQUENCE 20 AA; 2108 MW; 2BC7A93D022A97D8 CRC64;	
SQ	Query Match Similarity 28.6%; Score 24; DB 1; Length 20; Best Local Similarity 30.8%; Pred. No. 3.8e+02; Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps
QY 1 VLLKEFTVSGNLTIR 13	
Db 3 ILQDEYLSSGGVV 15	
RESULT 5	
ID APC1_MACFA STANDARD; PRT; 22 AA.	
AC P16657;	
RP SEQUENCE. MEDLINE=871185451; PubMed=3105581;	
RA Kantor P.N., Bauderman L.L., Lynch K.M., Saritelli A.L., Kantor M.A., Nicolosi R.J., Shulman R.S.;	
RT "Homologues of the human C and A apolipoproteins in the Macaca fasciularis (cynomolgus monkey)."; Biochemistry 26:1457-1463(1987).	
RL DE APC1_MACFA C1-I (APO-C1) (FRAGMENT).	
OS Macaca fasciularis (Crab eating macaque) (Cynomolgus monkey).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buthieria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.	
CC NCBI_TAXID=9341; [1]	
RP SEQUENCE.	
RX MEDLINE=871185451; RA Kantor P.N., Bauderman L.L., Lynch K.M., Saritelli A.L., Kantor M.A., Nicolosi R.J., Shulman R.S.;	
RT "Homologues of the human C and A apolipoproteins in the Macaca fasciularis (cynomolgus monkey)."; Biochemistry 26:1457-1463(1987).	
RL DE APC1_MACFA C1-I (APO-C1) (FRAGMENT).	
CC -1 FUNCTION: APPEARS TO MODULATE THE INTERACTION OF APOE WITH BETA-MIGRATING VLDL AND INHIBIT BINDING OF BETA-VLDL TO THE LDL RECEPTOR RELATED PROTEIN.	
CC -1 SUBCELLULAR LOCATION: EXTRACELLULAR.	
CC -1 TISSUE SPECIFICITY: SECRETED IN PLASMA.	
CC -1 MISCELLANEOUS: APO-C1 MAKES UP ABOUT 10% OF THE PROTEIN OF THE VLDL (VERY LOW DENSITY LIPOPROTEIN) & 28% OF THAT OF HDL (HIGH DENSITY LIPOPROTEIN).	
CC -1 SIMILARITY: BELONGS TO THE APOC1 FAMILY.	

DR PIR; C26627; C26627.
 DR HSSP; P02654; Iopp.
 KW Plasma; Lipid transport; VLDL.
 FT NON_TER SEQUENCE 22 AA; 22 MW; 4E478A03C91EA914 CRC64;

Query Match Similarity 28.0%; Score 23.5; DB 1; Length 22;
 Best Local Similarity 63.6%; Pred. No. 5.2e+02; Mismatches 0; Indels 1; Gaps 1;

Matches 7; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 3 LKEFTVSGNLT 13
 Db 11 LREF--GNTL 18

RESULT 6

FLB3_TREHY ID FLB3_TREHY STANDARD: PRT; 25 AA.
 AC P80161;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE FLAGELLAR FILAMENT CORE PROTEIN FLAB3 (32 KDA CORE PROTEIN)
 DE (FRAGMENT).
 GN FLAB3.
 OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
 OC Bacteria; Spirochaetales; Brachyspiraceae; Brachyspira.
 NCBI_TaxID=159; [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C5;
 RX MEDLINE=93139764; PubMed=1487733;
 RA Koopman M.B.H., Baets E., van der Zeijst B.A.M., Kusters J.G.;
 RA van der Zeijst B.A.M., Kusters J.G.;
 RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are composed of two sheath proteins and three core proteins."
 RL J. Gen. Microbiol. 138:2697-2706(1992).
 CC 1- FUNCTION: COMPONENT OF THE CORE OF THE FLAGELLA.
 CC -1- SUBUNIT: OUTER LAYER IS COMPOSED OF TWO SHEATH PROTEINS, FLAAL (44 KDa) AND FLA2 (35 KDa) AND A CORE THAT CONTAINS THREE PROTEINS FLAB1 (37 KDa), FLAB2 (34 KDa) AND FLAB3 (32 KDa).
 CC 2- SUBCELLULAR LOCATION: PERIPLASMIC FLAGELLUM.
 CC 3- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 DR PIR; D47689; D47689.
 KW Flagella; Periplasmic.
 FT NON_TER SEQUENCE 25 AA; 25 MW; 1AAA0CA722EE3D0A CRC64;

Query Match Similarity 27.4%; Score 23; DB 1; Length 25;
 Best Local Similarity 27.3%; Pred. No. 7.3e+02; Mismatches 5; Indels 0; Gaps 0;

Matches 3; Conservative 27.3%; Mismatches 3; Indels 0; Gaps 0;

Qy 4 KEFTVSGNLT 14
 Db 14 RQLNLTGNSMT 24

RESULT 7

KORA_METTM ID KORA_METTM STANDARD: PRT; 20 AA.
 AC P80904;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE OXIDOREDUCTASE SUBUNIT (KORA) (EC 1.2.7.3) (2-KETOGlutARATE OXIDOREDUCTASE ALPHA CHAIN) (KOR) (2-OXOGlutARATE-FERREDOXIN KORA).
 DE OXIDOREDUCTASE ALPHA SUBUNIT (FRAGMENT).
 GN KORA.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriaceae;
 OC Methanothermobacter.

OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97261844; PubMed=9108258;
 RA Tersteeden A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of fur anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum.";
 RT Eur. J. Biochem. 244:862-868(1997).
 CC -1- CATALYTIC ACTIVITY: 2-OXOBUTANATE + COA + OXIDIZED FERREDOXIN = PROPANOYL-COA + CO(2) + REDUCED FERREDOXIN.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE KORA, KORB, KORC AND KORD SUBUNITS.
 CC -1- MISCELLANEOUS: THE PH OPTIMUM IS PH 9.0 AND THE OPTIMAL TEMPERATURE IS 70 DEGREES CELSIUS.
 KW Oxidoreductase.
 FT NON_TER SEQUENCE 20 AA; 20 MW; 112E7E0E4AC76B76 CRC64;

OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97261844; PubMed=9108258;
 RA Tersteeden A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of fur anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum.";
 RT Eur. J. Biochem. 244:862-868(1997).
 CC -1- CATALYTIC ACTIVITY: 2-OXOBUTANATE + COA + OXIDIZED FERREDOXIN = PROPANOYL-COA + CO(2) + REDUCED FERREDOXIN.
 CC -1- SUBUNIT: HETEROTETRAMER OF THE KORA, KORB, KORC AND KORD SUBUNITS.
 CC -1- MISCELLANEOUS: THE PH OPTIMUM IS PH 9.0 AND THE OPTIMAL TEMPERATURE IS 70 DEGREES CELSIUS.
 KW Oxidoreductase.
 FT NON_TER SEQUENCE 20 AA; 20 MW; 112E7E0E4AC76B76 CRC64;

RESULT 8

LPR_BACST ID LPR_BACST STANDARD: PRT; 20 AA.
 AC P06558;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TETRACYCLINE RESISTANCE LEADER PEPTIDE.
 GN TEPL.
 OS Bacillus stearothermophilus, Bacillus cereus, and Staphylococcus hyicus.
 OG Plasmid pTHT15, Plasmid pBC16, and Plasmid pSTE1.
 OC Bacterium; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 NCBI_TaxID=1422, 1396, 1284;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID=pTHT15;
 RX MEDLINE=86031344; PubMed=2996983;
 RA Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pTHT15, a thermophilic Bacillus plasmid: comparison with staphylococcal TCR controls.";
 RT Gene 37:131-138(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC PLASMID=pBC16;
 RX MEDLINE=90221899; PubMed=2109312;
 RA Palva A., Viigren G., Simonen M., Rintala H., Laamanen P.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pBC16 from Bacillus cereus.";
 RT Nucleic Acids Res. 18:1635-1635(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.hylcus; PLASMID=pSTE1;
 RX MEDLINE=92321725; PubMed=1622166;
 RA Schwarz S., Cardoso M., Wegener H.C.;
 RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline resistance determinant encoded by plasmid pSTE1 from Staphylococcus hylicus.";
 RT AnImicrob. Agents Chemother. 36:580-588(1992).
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DR EMBL; D00006; BAA0004_1; -;
 DR EMBL; M1036; AAA2850..1.; -;
 DR EMBL; X51366; CAA5750..1.; -;
 DR EMBL; X0828; CAA13219..1.; -;
 DR PIR; S0933; LFBSTU.
 DR PIR; S23742; S23742.
 KW Leader peptide; Antibiotic resistance; Plasmid.
 SQ SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA231CA1 CRC64;

Query Match 26.2%; Score 22; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 8.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 VILKEFTVS 9
 | | | | :| |
 Db 9 VQLKEGSVS 17

RESULT 9
 LPTR_BACSU LPTR_BACSU STANDARD; PRT; 20 AA.
 AC P2353;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE TETRACYCLINE RESISTANCE LEADER PEPTIDE.
 GN TETL.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 SEQUENCE FROM N.A.
 STRAIN=168;
 RX MEDLINE=89000797; PubMed=2844262;

RA Sataguchi R., Amano H., Shishido K.;
 "Nucleotide sequence homology of the tetracycline-resistance determinant naturally maintained in *Bacillus subtilis* Marburg 168 chromosome and the tetracycline-resistance gene of *B. subtilis* plasmid pNS1981.";
 RL Biophys. Acta 950:441-444(1998).
 RN [2]
 SEQUENCE FROM N.A.
 MEDLINE=91257555; PubMed=1646143;
 RA "An insertion of *Escherichia coli* transposon element IS1K into the site immediately before tetracycline-resistance determinant of *Bacillus subtilis* chromosomal DNA fragment in cloning in *E. coli*.";
 RT FEMS Microbiol. Lett. 63:5-8(1991).
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DR EMBL; X08034; CAA10826..1.; -;
 DR EMBL; X88999; CAA41744..1.; -;
 DR PIR; S0802; LFBSTU.
 DR PIR; S17282; S17282.
 DR SubList; BG11051; tetL.
 KW Leader Peptide; Antibiotic resistance.
 SQ SEQUENCE 20 AA; 2298 MW; E870F516CA23111A CRC64;

<p>CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).</p> <p>DR EMBL; D00006; BAA0004_1; -; DR EMBL; M1036; AAA2850..1.; -; DR EMBL; X51366; CAA5750..1.; -; DR EMBL; X0828; CAA13219..1.; -; DR PIR; S0933; LFBSTU. DR PIR; S23742; S23742. KW Leader peptide; Antibiotic resistance; Plasmid. SQ SEQUENCE 20 AA; 2253 MW; 18D0F4A6CA231CA1 CRC64;</p> <p>Query Match 26.2%; Score 22; DB 1; Length 20; Best Local Similarity 66.7%; Pred. No. 8.6e+02; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;</p> <p>Qy 1 VILKEFTVS 9 : Db 9 VQLKEGSVS 17</p> <p>RESULT 10 TPX_CLOPA TPX_CLOPA STANDARD; PRT; 20 AA.</p> <p>ID TPX_CLOPA AC P81361; DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 15-JUL-1998 (Rel. 36, Last annotation update)</p> <p>DE PROBABLE THIOL PEROXIDASE (EC 1.11.1.) (CP 42) (FRAGMENT).</p> <p>OS Clostridium pasteurianum.</p> <p>OC Bacteria; Firmicutes; Bacillales/Clostridium group; Clostridiaceae; Clostridium.</p> <p>OX NCBI_TaxID=1501;</p> <p>RN [1] RP SEQUENCE.</p> <p>RC STRAIN=W5; RX MEDLINE=98291870; PubMed=96299918; RA Flengstrud R., Skjeldal L.; "Two-dimensional gel electrophoresis separation and N-terminal sequencing analysis of proteins from <i>Clostridium pasteurianum</i> W5."; RL Electrophoresis is 19:802-806(1998). -!- FUNCTION: HAS ANTI-OXIDANT ACTIVITY. COULD REMOVE PEROXIDES OR H2O2(O2) (BY SIMILARITY). CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: CC 4.6, ITS MW IS: 20.2 kDa. CC -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. TPX SUBFAMILY. DR InterPro; IPR002065; -. DR PROSITE; PS01265; TPX; PARTIAL. KW Oxidoreductase; Peroxidase. FT NON-TER 20 SQ SEQUENCE 20 AA; 2193 MW; 08178FC2D782E765 CRC64;</p> <p>Query Match 26.2%; Score 22; DB 1; Length 20; Best Local Similarity 40.0%; Pred. No. 8.6e+02; Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;</p> <p>Qy 7 TVSGNLTIR 16 : : Db 4 TFQGNEVTLQ 13</p> <p>RESULT 11 FLAL_SULSH FLAL_SULSH STANDARD; PRT; 23 AA.</p> <p>ID FLAL_SULSH AC Q9W6G6; DT 01-OCT-2000 (Rel. 40, Created) DT 01-OCT-2000 (Rel. 40, Last sequence update)</p> <p>DE 31/33 KDA FLAGELLIN (FRAGMENT).</p> <p>OS Sulfolobus shibatae.</p> <p>OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.</p> <p>OX NCBI_TaxID=2286;</p> <p>RN [1] RP SEQUENCE.</p> <p>RC STRAIN=FB12; RX MEDLINE=96146545; PubMed=8550530;</p> <p>RA Faguy D.M., Bayley D.P., Kostyukova A.S., Thomas N.A., Jarrell K.F.;"Isolation and characterization of flagella and flagellar proteins from the Thermoacidophilic archaea <i>Sulfolobus volvulum</i> and <i>Sulfolobus shibatae</i>." RT J. Bacteriol. 178:902-905(1996). CC -!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLIMERIZES TO FORM THE FILAMENTS OF FLAGELLA.</p>

CC -!- PTM: GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE ARCHAEBAL FLAGELLIN FAMILY.
 KW Flagella; Glycoprotein.
 FT NON_TER 23 23 MW: BB372157B44DB3AC CRC64;
 SQ SEQUENCE 23 AA: 2362 MW: BB372157B44DB3AC CRC64;

Query Match 26.28; Score 22; DB 1; Length 23;
 Best Local Similarity 23.18; Pred. No. 9.9e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 RT
 QY 1 VLLKEFTVSGN1 13
 DB 8 ILLIAFLITASVL 20

RESULT 12
 TPIS_NICPL STANDARD PRT; 10 AA.

ID TPIS_NICPL
 AC P19118;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (EC 5.3.1.1) (TIM) (FRAGMENT).
 OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 NCBI_TAXID=4092;
 RN [1]
 RP

SEQUENCE.
 RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerchhove J.;
 RT "Alterations in the phenotype of plant cells studied by NH2-terminal
 amino acid-sequence analysis of proteins electroblotted from two-
 dimensional gel-separated total extracts";
 RR Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
 CC -!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE = DIHYDROXY-
 ACETONE PHOSPHATE.
 CC -!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CITOPLASMIC (PROBABLE).
 CC -!- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
 AND PLASTID.
 CC -!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
 DR PIR: A27617; A27617.
 DR InterPro; IPR00052; -.
 DR PROSITE; PS00171; TIM; PARTIAL.
 KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
 KW Pentose shunt.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1140 MW: 8059D37062C9C9D1 CRC64;

Query Match 25.0%; Score 21; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6e+02; Indels 3; Gaps 0;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 13
 OPSS3_DROVI STANDARD PRT; 12 AA.

QY 4 KFFTVSGN 11
 DB 2 RFFFVGGN 9

RESULT 13
 OPSS3_DROVI STANDARD PRT; 12 AA.
 AC P17645;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE OPIN RH3 (INNER R7 PHOTORECEPTOR CELLS OPSIN) (FRAGMENT).
 GN RH3.
 OS Drosophila virilis (Fruit fly).
 OC Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Blaberoidea; Blaberidae; Leucophaea.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Blaberoidea; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 NCBI_TAXID=6988;
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Brain;
 RX MEDLINE=91269266; PubMed=9114474;
 RA Muren J.E., Naezel D.R.;
 RT "Seven tachakinin-related peptides isolated from the brain of the

RT madeira cockroach; evidence for tissue-specific expression of
 RT isoforms.
 RL Peptides 18:7-15(1997);
 CC -!- TISSUE SPECIFICITY: BRAIN.
 CC -!- MASS SPECTROMETRY: MW=1435.7; METHOD=MALDI-MS.
 SQ SEQUENCE 13 AA; 1436 MW; 8E532C9DE3A7D1B5 CRC64;

Query Match 25 0%; Score 21; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 8e+02;
 Matches 5; conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 LLKEFTVS 9
 | : | 1 |
 Db 2 LFEEESTVS 9

RESULT 15
 CDN3_LITGI STANDARD PRT; 15 AA.
 ID _CDN3_LITGI PRT; 15 AA.
 AC P56248;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CAERIDIN 3.
 OS Litoria gilleni.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 RN [1] NCBI_TAXID=39405;
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 WAugh R.J., Stoen D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins and
 caeridins from *Litoria gilleni*."
 RT *J. Chem. Res.* 139:947-961(1993).
 CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.
 CC -!- MASS SPECTROMETRY: MW=1428; METHOD=FAB.
 KW Amphibian skin; Amidation.
 FT MOD_RES 15 15 AMIDATION.
 SQ SEQUENCE 15 AA; 1430 MW; 06E90A79AF70CBF CRC64;

Query Match 25 0%; Score 21; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 6 FFWGNIL 13
 | : |
 Db 3 FDAGNL 10

Search completed: May 8, 2001, 15:14:07
 Job time: 528 sec

Gencore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.
4 protein - protein search, using SW model
 on on: May 8, 2001, 15:16:05 ; Search time 114.89 Seconds
 (without alignments)
 18.363 Million cell updates/sec

title: US-09-165-546A-9
 perfect score: 84
 sequence: VLLKETVSGNLITRLT 18
 scoring table: BLOSUM62
 Gapext 0.5
 searched: 374700 seqs, 117207915 residues
 total number of hits satisfying chosen parameters: 6627

minimum DB seq length: 0
 maximum DB seq length: 25
 post-processing: Minimum Match 0%

P82399 litoria aur
 Q16475 homo sapien
 Q9umb2 homo sapien
 Q88717 mus musculus
 Q9yn05 myxoma virus
 Q9pxh2 human t-cell
 Q9qyf6 mus musculus
 Q92901 rhizobium m
 Q9prq0 oncosynchus
 Q31213 mus musculus
 O24445 ceratodon purpureus
 O9ih09 human polio
 O9ih10 human polio
 O9ih19 human polio
 O9ih18 human polio
 O9ih17 human polio
 O9ih16 human polio
 O9ih15 human polio
 O9ih14 human polio
 O9ih13 human polio
 O9ih12 human polio
 O9ih11 human polio
 O9ih10 human polio
 O9ihh9 human polio
 O9ihh8 human polio
 O9ihh7 human polio
 O9ihh6 human polio

ALIGNMENT S

	RESULT	1
	Q9R4Y1	PRELIMINARY;
2:	ID	Q9R4Y1;
3:	AC	Q9R4Y1;
4:	DT	01-MAY-2000 (TREMBLrel. 13, Created)
5:	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
6:	SP	sp_mhc_*
7:	SP	sp_invertebrate:_*
8:	SP	sp_mammal:_*
9:	SP	sp_organelle:_*
10:	SP	sp_phage:_*
11:	SP	sp_plant:_*
12:	SP	sp_rooted:_*
13:	SP	sp_unclassified:_*
14:	SP	sp_vertibrate:_*
14:	RN	NCBI_TaxID=585;
	RN	[1]
	RN	RP SEQUENCE;
	RX	MEDLINE=94298804; PubMed=8026480;
	RA	Trautwein T., Krauss F., Lotspeich F., Simon H.;
	RT	"The (2R)-hydroxy-carboxylate-viologen-oxidoreductase from Proteus vulgaris is a molybdenum-containing iron-sulphur protein.",
	RT	Eur. J. Biochem. 222:105-102(1994).
	RL	SEQUENCE 20 AA; D12ACFC51207C63 CRC64;
	SC	2145 MW;
	RESULT	2
	Q9TR36	PRELIMINARY;
1	ID	Q9TR36;
2	AC	Q9TR36;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	PHOSPHATIDYLINOSTEROL-TRANSFER PROTEIN 36 KDA ISOFORM (FRAGMENT).
6	OS	Bos taurus (Bovine).
7	OC	Mammalia; Eutheria; Chordata; Craniota; Ruminantia; Pecora; Bovidae.
8	OC	
	RESULT	3
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	4
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	5
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	6
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	7
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	8
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	9
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	10
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	11
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	12
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	13
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	14
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	15
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	16
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	17
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	18
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	19
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	
	RESULT	20
	Q9R4Y1	PRELIMINARY;
1	ID	Q9R4Y1;
2	AC	Q9R4Y1;
3	DT	01-MAY-2000 (TREMBLrel. 13, Created)
4	DT	01-JUN-2000 (TREMBLrel. 14, Last sequence update)
5	DE	(2R)-HYDROXYCARBOXYLATE-VILOGEN-OXIDOREDUCTASE (FRAGMENT).
6	OS	Proteus vulgaris.
7	OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
8	OC	Proteus.
9	OC	

OC Bovidae; Bovinae; Bos. OX NCBI_TaxID=9913; RN [1] RP SEQUENCE; MEDLINE=95382786; PubMed=7654206; RX de Vries K.J., Henrichs A.A., Cunningham E., Brunink F., Wirtz K.W., Snoek G.T.; RA Westerman J., Somerharju P.J., Cockcroft S., Wirtz K.W., Snoek G.T.; RT "An isoform of the phosphatidylinositol-transfer protein transfers sphingomyelin and is associated with the Golgi system."; RL Biochem. J. 310:643-649 (1995). DR INTERPRO; IPR01666; -; PFAM; PF02121; IP_trans; 1. SQ SEQUENCE 21 AA; 2442 MW; 0978BC2B0067EF0E CRC64;	RX MEDLINE=98047369; PubMed=9385145; RA Shi L., Carmichael W.W.; RT "PPI-cyano2, a protein serine/threonine phosphatase 1 gene from the cyanobacterium Microcystis aeruginosa UTEX 2063."; RL Arch. Microbiol. 168:528-531 (1997). DR EMBL; AF037161; AAC46049.1; -; DR INTERPRO; IPR00934; -; DR PFAM; PF00149; Stphosphatase; 1. FT NON-TER 1 FT NON-TER 24 24 SQ SEQUENCE 24 AA; 2768 MW; DB9C36D51C0DA51D CRC64;
Query Match 34.5%; Score 29; DB 6; Length 21; Best Local Similarity 75.0%; Pred. No. 2.8e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Query Match 34.5%; Score 29; DB 2; Length 24; Best Local Similarity 60.0%; Pred. No. 3.3e+02; Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 VLKEFTV 8 Db 1 VLKEFV 8 Db 1 VLKEFRV 8	Qy 2 LLKEFTVSGN 11 Db 5 LLKLFEVGN 14
RESULT 5 Q9TR37	RESULT 5 Q9TR37
ID Q9TR37 PRELIMINARY; PRT; 21 AA. AC Q9TR37; PRELIMINARY; PRT; 21 AA. DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update) DE PHOSPHATIDYLINOSITOL-TRANSFER PROTEIN 35 KDA ISFORM (FRAGMENT). OS Bos taurus (Bovine). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Peccra; Bovoidea; Bovidae; Bovinae; Bos. OX NCBII_TaxID=9913; RN [1] RP SEQUENCE.	ID Q9TR37 PRELIMINARY; PRT; 21 AA. AC Q9TR37; PRELIMINARY; PRT; 21 AA. DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-JUN-2000 (TREMBLrel. 13, Last sequence update) DE PHOSPHATIDYLINOSITOL-TRANSFER PROTEIN 35 KDA ISFORM (FRAGMENT). OS Bos taurus (Bovine). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Peccra; Bovoidea; Bovidae; Bovinae; Bos. OX NCBII_TaxID=9913; RN [1] RP SEQUENCE.
Query Match 34.5%; Score 29; DB 6; Length 22; Best Local Similarity 55.6%; Pred. No. 3e+02; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	Query Match 33.3%; Score 28; DB 6; Length 21; Best Local Similarity 75.0%; Pred. No. 4.2e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LLKEFTVSG 10 Db 6 IAKESVNG 14	Qy 1 VLKEFTV 8 Db 1 VLKEYRV 8
RESULT 6 Q9TR5	RESULT 6 Q9TR5
ID Q9TR5 PRELIMINARY; PRT; 20 AA. AC Q9TR5; PRELIMINARY; PRT; 20 AA. DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DE FACTOR IX LIGHT CHAIN (GLA DOMAIN). OS Oryctolagus cuniculus (Rabbit). OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. OX NCBII_TaxID=9986; RN [1] RP SEQUENCE. RX MEDLINE=92132840; PubMed=1776139; RA Rao L.V., Hoang A.D.;	ID Q9TR5 PRELIMINARY; PRT; 20 AA. AC Q9TR5; PRELIMINARY; PRT; 20 AA. DT 01-OCT-2000 (TREMBLrel. 13, Created) DT 01-OCT-2000 (TREMBLrel. 13, Last sequence update) DE FACTOR IX LIGHT CHAIN (GLA DOMAIN). OS Oryctolagus cuniculus (Rabbit). OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. OX NCBII_TaxID=9986; RN [1] RP SEQUENCE. RX MEDLINE=92132840; PubMed=1776139; RA Rao L.V., Hoang A.D.;
Query Match 34.5%; Score 29; DB 2; Length 22; Best Local Similarity 55.6%; Pred. No. 3e+02; Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	Query Match 33.3%; Score 28; DB 6; Length 21; Best Local Similarity 75.0%; Pred. No. 4.2e+02; Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LLKEFTVSG 10 Db 6 IAKESVNG 14	Qy 1 VLKEFTV 8 Db 1 VLKEYRV 8

RP "Purification and characterization of rabbit factor IX and its
RT existence as a two-chain factor IX alpha in circulating plasma.";
RL Thromb. Res. 64:67-68(1991).
DR PMID: 100740; ICH.
SQ SEQUENCE 20 AA; 2317 MN; 9368E94B44BF5800 CRC64;

Query Match 32.7% Score 27.5; DB 6; Length 20;
Best Local Similarity 70.0%; Pred. No. 4.9e+02; Indels 1; Gaps 1;

RESULT 7 Q9UWH9 PRELIMINARY; PRT; 15 AA.

Qy 3 LKEFTVSGNI 1.2
Db 6 LEFF-VSGNL 1.4

Q9UWH9 AC Q9UWH9; PRELIMINARY; PRT; 15 AA.
ID 01-MAY-2000 (TREMBLrel. 13 Created)
DT 01-MAY-2000 (TREMBLrel. 13 Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14 Last annotation update)
DE ALDEHYDE FERRODOXIN OXIDOREDUCTASE (FRAGMENT).
OS Thermococcus sp. (strain 90N-7).
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae.
OX NCBI_TAXID=2263;
RN [1]
RP SEQUENCE.
RX MEDLINE=95370155; PubMed=7642503;
RA Heider J.; Ma K.; Adams M. W.;
RT "Purification, characterization, and metabolic function of tungsten-containing aldehyde ferredoxin oxidoreductase from the hyperthermophilic and protoarchaeal archaeon Thermococcus strain ES-1.";
RU J. Bacteriol. 177:4757-4764(1995).
SQ SEQUENCE 15 AA; 1750 MN; 0441670278198619 CRC64;

Query Match 32.1% Score 27; DB 1; Length 15; Best Local Similarity 46.2%; Pred. No. 4.4e+02; Indels 6; Gaps 0;	RESULT 9 P92152 PRELIMINARY; PRT; 24 AA.
Qy 3 LKEFTVSGNI 1.2 Db 6 LEFF-VSGNL 1.4	Qy 2 LLKEFTVSGNLTIR 18 Db 3 IVKGESPGRDLSVKET 19
Q9UWH9 AC Q9UWH9; PRELIMINARY; PRT; 15 AA. ID 01-MAY-2000 (TREMBLrel. 13 Created) DT 01-MAY-2000 (TREMBLrel. 13 Last sequence update) DT 01-JUN-2000 (TREMBLrel. 14 Last annotation update) DE ALDEHYDE FERRODOXIN OXIDOREDUCTASE (FRAGMENT). OS Thermococcus sp. (strain 90N-7). OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae. OX NCBI_TAXID=2263; RN [1] RP SEQUENCE. RX MEDLINE=95370155; PubMed=7642503; RA Heider J.; Ma K.; Adams M. W.; RT "Purification, characterization, and metabolic function of tungsten-containing aldehyde ferredoxin oxidoreductase from the hyperthermophilic and protoarchaeal archaeon Thermococcus strain ES-1."; RU J. Bacteriol. 177:4757-4764(1995). SQ SEQUENCE 15 AA; 1750 MN; 0441670278198619 CRC64;	Q9UWH9 AC Q9UWH9; PRELIMINARY; PRT; 15 AA. ID 01-MAY-2000 (TREMBLrel. 13 Created) DT 01-MAY-2000 (TREMBLrel. 13 Last sequence update) DT 01-OCT-2000 (TREMBLrel. 15 Last sequence update) DE PARVALBUMIN (FRAGMENT). OS Bos taurus (Bovine). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Bovidae; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; OC Bovinae; Bos. ON NCBI_TAXID=9913; RN [1] RP SEQUENCE FROM N.A. RA Ariza F.; Harrison B.; Drinkwater R.; RT "The Assignment by Linkage Mapping of Five Genes from Human Chromosome 22 to Bovine Chromosome 5, 14 and 17."; RU Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. FT NON-TER 1 1 SQ SEQUENCE 19 AA; 2151 MN; D5EA9D89BC3BE951 CRC64;
Query Match 31.0% Score 26; DB 6; Length 19;	Query Match 31.0% Score 26; DB 6; Length 19;
	Qy 3 LKEFTVSGN 11

Db 10 LKEF - AGVVV 19

RESULT 15
 Q9TY69 PRELIMINARY; PRT; 24 AA.
 ID Q9TY69;
 AC ;
 DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13; Created)
 DT 01-OCT-2000 (TREMBLrel. 15; Last annotation update)
 DE PROTEIN PHOSPHATASE FROM PCR FRAGMENT D14 (FRAGMENT).
 GN Ppd14.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TAXID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:9233178; PubMed=1321058;
 RA Chen M.X., Chen Y.H., Cohen P.T.;
 RT "Polymerase chain reactions using Saccharomyces, Drosophila and human
 DNA predict a large family of protein serine/threonine phosphatases.";
 RU FEBS Lett. 306:54-58(1992).
 EMBL: S39996; AAB24466.1;
 DR HSSP; P08129; 1FJ.M.
 DR FLYBASE; FBgn0005780; Ppd14.
 DR IPR000934;
 DR PFAM; PF00149; Stphosphatase_1.
 FT NON_TER 1 1
 SEQUENCE 24 AA; 2716 MW; 9746395CC1E7FBB CRC64;

Query Match 29.88; Score 25; DB 5; Length 24;
 Best Local Similarity 46.7%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 7;

Oy 2 LKKEFTVSGNLTIR 16
 | : | | | | | | | |
 Db 5 LVKLFEVGGPPATTR 19

Search completed: May 8, 2001, 15:16:06
 Job time: 532 sec

GenCore version 4.5				
Copyright (c) 1993 - 2000 Compugen Ltd.				
(Protein - protein search, using sw model				
in on: May 8, 2001, 15:07:08 ; Search time 113.31 Seconds (without alignments) 9.081 Million cell updates/sec				
title: US-09-165-546A-11				
perfect score: 105				
Sequence: 1 GRASGNGCCRCGARGPGE 18				
Scoring table: BLOSUM62				
Gapop 10.0 , Gapext 0.5				
searched: 390729 seqs, 5716335 residues				
Total number of hits satisfying chosen parameters:	165078			
Minimum DB seq length: 0				
Maximum DB seq length: 25				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 45 summaries				
database :				
A_Geneseq_0401:*				
1: /SIDSS6/gcdata/geneseq/geneseqp/AA1980.DAT:*				
2: /SIDSS6/gcdata/geneseq/geneseqp/AA1981.DAT:*				
3: /SIDSS6/gcdata/geneseq/geneseqp/AA1982.DAT:*				
4: /SIDSS6/gcdata/geneseq/geneseqp/AA1983.DAT:*				
5: /SIDSS6/gcdata/geneseq/geneseqp/AA1984.DAT:*				
6: /SIDSS6/gcdata/geneseq/geneseqp/AA1985.DAT:*				
7: /SIDSS6/gcdata/geneseq/geneseqp/AA1986.DAT:*				
8: /SIDSS6/gcdata/geneseq/geneseqp/AA1987.DAT:*				
9: /SIDSS6/gcdata/geneseq/geneseqp/AA1988.DAT:*				
10: /SIDSS6/gcdata/geneseq/geneseqp/AA1990.DAT:*				
11: /SIDSS6/gcdata/geneseq/geneseqp/AA1991.DAT:*				
12: /SIDSS6/gcdata/geneseq/geneseqp/AA1992.DAT:*				
13: /SIDSS6/gcdata/geneseq/geneseqp/AA1993.DAT:*				
14: /SIDSS6/gcdata/geneseq/geneseqp/AA1994.DAT:*				
15: /SIDSS6/gcdata/geneseq/geneseqp/AA1995.DAT:*				
16: /SIDSS6/gcdata/geneseq/geneseqp/AA1996.DAT:*				
17: /SIDSS6/gcdata/geneseq/geneseqp/AA1997.DAT:*				
18: /SIDSS6/gcdata/geneseq/geneseqp/AA1998.DAT:*				
19: /SIDSS6/gcdata/geneseq/geneseqp/AA1999.DAT:*				
20: /SIDSS6/gcdata/geneseq/geneseqp/AA2000.DAT:*				
21: /SIDSS6/gcdata/geneseq/geneseqp/AA2001.DAT:*				
22: /SIDSS6/gcdata/geneseq/geneseqp/AA2002.DAT:*				
Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
8				
Result No.	Score	Match Length	DB ID	Description
1	105	100 0	18 21	Y52438 Human tumour antigen
2	64	61 0	10 20	Y06012 Human cancer antigen
3	63	60 0	10 20	Y06063 Human cancer antigen
4	63	60 0	10 20	Y06008 Human cancer antigen
5	59	56 2	9 20	Y06044 Human cancer antigen
6	57	54 3	10 20	Y06060 Human cancer antigen
7	57	54 3	10 20	Y05994 Human cancer antigen
8	53	50 5	9 20	Y06047 Human cancer antigen
9	47	44 8	10 20	Y06059 Human cancer antigen
10	47	44 8	10 20	Y06092 Human cancer antigen
11	40 0	40 0	10 14	R69313 GP IIB/IIIa receptor
				DR WPI: 20000-03B483/03 .
ALIGMENTS				
RESULT 1				
Y52438	ID	Y52438 standard, Protein, 18 AA.		
XX				
AC Y52438;				
XX				
DT 15-FBB-2000 (first entry)				
DE Human tumour antigen NY-ESO-1 peptide #11.				
XX				
Cancer; tumour antigen; MHC: major histocompatibility complex; Class II; T-cell; helper; stimulation; proliferation; treatment; diagnosis; prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; KW lymphoma.				
OS Synthetic.				
OS Homo sapiens.				
XX				
PN WO9933938-A1.				
XX				
XX				
PD 28-OCT-1999.				
XX				
PP 24-MAR-1999;				99WO-US06675.
XX				
PR 17-APR-1998;				98US-0062422.
XX				
PR 02-OCT-1998;				98US-016546.
XX				
PA (LUDWIG) LUDWIG INST CANCER RES.				
XX				
PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old L J, Gure A, Ritter G;				
DR				

X Novel peptides which bind to MHC class I and MHC class II molecules,
T useful for therapeutic and diagnostic purposes -
X
X Claim 4: Page 22; 49pp; English.
X Peptides #8-#13 (Y52435-Y52440) are peptides derived from the human
T T antigen, NY ESO-1 (Y52430) which can bind to MHC major
histocompatibility Class II HLA-DR53 molecules, thereby stimulating
proliferation of helper T-cells. cDNA encoding NY ESO-1 was initially
isolated from an oesophagus squamous cell cancer cDNA library. Tissue
localisation studies revealed it to be expressed at high levels
in normal ovary and testis, but not in normal colon, kidney, liver,
brain, oesophagus and skin. It was expressed in certain tumours and
tumour cell lines with some degree of frequency - these included
melanoma specimens and cell lines, and breast and bladder cancer
specimens, with expression in other tumour types being sporadic.
These NY ESO-1-derived peptides may be used in methods and
compositions used for the treatment, diagnosis and prevention of
cancers (such as melanoma, breast cancer, prostate cancer, lung
cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
or lymphoma) and to stimulate the proliferation of T cells.

This peptide was identified as an HUA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y03988-106017) were identified. The present peptide (ranked 25) corresponds to amino acid residues 71-80 of CAG-1 ORF1 (see Y05695). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer Peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

		Query Match	100.0%	Score 105;	DB 21;	Length 18;			
		Best Local Similarity	100.0%	Pred. No. 2.5e-07;					
X		Conservative Matches	18;	Mismatches 0;					
				Indices 0;					
				Gaps 0;					
Sequence	18 AA;								
Y		1 GAASGLNGCRCRGPE	18						
Z		1 aaasglnacccggare	18						

RESULT 2
00012 10.8%
00013 10.8%
00014 10.8%
00015 10.8%
00016 10.8%

vaccine; human leukocyte antigen; DNA.

X WO9918206-A2 .
X 15-APR-1999 .
X 21-SEP-1998 ; 98WO-US19609.
X 08-OCT-1997 ; 97US-0061428.

(USSH) US DEPT HEALTH & HUMAN SERVICES
Rosenberg SA, Wang RF;
WPT: 1999-277270/23.
Cancer antigen NY ESO1/CAG-3
Example 10; Page 42; 88pp; English.

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X55599). 30 Epitopes (see Y05988-Y06017) were identified. The present peptide (ranked 25) corresponds to amino acid residues 71-80 of CAG-1 ORF1 (see Y05865). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

	Sequence	Match	Query Match	Score	DB	Length	Indels	Gaps	0;
1	X	AA	Best Local Similarity	100.0%	DB-21;	Length 18;			
2	Y	AA	Matches	18;	Pred. No. 2.5e-07;	Mismatches 0;	0;	0;	0;
3	Z	AA	Matches	18;	Conservative	0;	0;	0;	0;
4			1	GAASGLNGCRCRGPE	18				
5			1						
6			1	qaasqinacrcgareone	18				

Human cancer antigen NY ESO-1/CAG-3 peptide ESO10-12.
NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; cytotoxic T lymphocyte; CTL.

WO9918206-A2

13-APR-1999.
21-SEP-1998;

08-OCT-1997; 97US-0061428.
(USSH) US DEPT HEALTH & HUMAN SERVICES.

Rosenberg SA, Wang RF;
WPI; 1999-277270/23.
Cancer antigen NY ESO1/CAG-3
Example 10; Page 45; 88pp; English.
Peptide ESO10-72 corresponds to amino acid residues 72-81 of human NY ESO-1/CAG-3 ORF1 (see Y05365) a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. It was examined for reactivity to a cytotoxic T lymphocyte (CTL), measured as release of granulocyte macrophage colony stimulating factor. Cancer peptides (see Y05967-87) derived

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 AC NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 XX non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 DF KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; colon cancer;
 XX metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 DE KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 XX cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 XX vaccine; cytotoxic T lymphocyte; CTL.
 XX Homo sapiens.
 OS XX Homo sapiens.
 PN XX WO9918206-A2.
 PD XX 15-APR-1999.
 PA XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PF XX 21-SEP-1998; 98WO-US19609.
 PR XX 08-OCT-1997; 97US-0061428.
 DR XX WPI: 1999-277270/23.
 PT XX Cancer antigen NY ESO1/CAG-3
 PS XX Example 10; Page 45; 88pp; English.
 XX Peptide ESO10-77 corresponds to amino acid residues 77-86 of
 CC human NY ESO-1/CAG-3 ORF1 (see Y05965), a new and potent tumour
 CC antigen capable of eliciting an antigen specific immune response
 CC by T cells. It was examined for reactivity to a cytotoxic T
 CC lymphocyte (CTL), measured as release of granulocyte macrophage
 CC colony stimulating factor. Cancer peptides (see Y05967-87) derived
 CC from CAG-3, portions of CAG-3 and their variants, are useful as
 CC cancer vaccines. A claimed method of preventing or inhibiting
 CC cancer involves administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.
 XX Sequence 10 AA;
 SQ XX Query Match 44.8%; Score 47; DB 20; Length 10;
 Best Local Similarity 10.0%; Pred. No. 3.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 11 RCGARGPE 18
 ID 111111 8
 DB 1 rrgargpe 8
 RESULT 10
 YY 05993
 ID Y05993 standard; Peptide; 10 AA.
 XX
 AC Y05993;
 XX XX 16-AUG-1999 (first entry)
 DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
 XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 ID NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 XX non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 DE liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;

XX Human cancer antigen NY ESO-1/CAG-3 peptide ESO10-77.

PS Claim 2; Page 28; 58pp; English.

XX The venom of predatory cone snails comprises relatively small
 CC peptides which are targetted to various neuromuscular receptors
 CC and may be equivalent in their pharmacological diversity to the
 CC alkaloids of plants or secondary metabolites of microorganisms.
 CC Several peptides have been characterised from Conus venoms. These
 CC include the alpha and mu conotoxins which target nicotinic
 CC acetylcholine receptors and muscle sodium channels respectively.
 CC Chronic or intractable pain as well as neuropathic pain is
 CC currently treated with a range of analgesic compounds. It is
 CC thought that the tau-conotoxins described could have applications
 CC as analgesic drugs and could be used for treating such acute,
 CC chronic and neuropathic pain as well as migraines.

XX Sequence 11 AA;

Query	Match	Score	DB	Length
Y97109	Best Local Similarity	39.0%	21	11;
ID Y97109	No. 24;			
XX	Matches 6;			
AC Y97109;	Conservative	0;		
XX	Mismatches	1;		
DT 22-DEC-2000	Indels	0;		
XX	Gaps	0;		
DE Tau conotoxin sequence.				
KW Conotoxin; chronic pain; neuropathic pain; acetylcholine; receptor;				
KW antagonist; analgesic; drug; peptide; tau; cone snail; Conus; venom;				
KW migraine; treatment; therapy.				
XX OS Conus marmoreus.				
NN WO200046371-A1.				
XX PD 10-AUG-2000.				
XX PF 04-FEB-2000; 2000WO-US03021				
XX PR 04-FEB-1999; 99US-0118642.				
XX PA (UTAH) UNIV UTAH RES FOUND				
PA (COGN-) COGNETIX INC.				
XX PI Walker C, Shetty R, Oliveira BM, Hooper D, Jacobsen R, Steele D;				
PI Jones RM;				
XX DR 2000-542489/49.				
XX PT Novel analgesic short peptides from predatory cone snails for treating				
PT acute, chronic and neuropathic pain and migraines				
XX PS Claim 25; Page 29; 58pp; English.				
XX PT Novel analgesic short peptides from predatory cone snails for treating				
acute, chronic and neuropathic pain and migraines				
XX PS Claim 25; Page 29; 58pp; English.				

CC thought that the tau-conotoxins described could have applications
 CC as analgesic drugs and could be used for treating such acute,
 CC chronic and neuropathic pain as well as migraines.

Query	Match	Score	DB	Length
Qy 7 NGCCRCG 13	Best Local Similarity	39.0%	21	11;
Db 1 ngccrag 7	Matches 6;	85.7%	24	1;
SQ Sequence 11 AA;	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;

Search completed: May 8, 2001, 15:07:10
 Job time: 226 sec

CC The venom of predatory cone snails comprises relatively small
 CC peptides which are targetted to various neuromuscular receptors
 CC and may be equivalent in their pharmacological diversity to the
 CC alkaloids of plants or secondary metabolites of microorganisms.
 CC Several peptides have been characterised from Conus venoms. These
 CC include the alpha and mu conotoxins which target nicotinic
 CC acetylcholine receptors and muscle sodium channels respectively.
 CC Chronic or intractable pain as well as neuropathic pain is
 CC currently treated with a range of analgesic compounds. It is

Copyright (c) 1993 - 2000 Compugen Ltd.	Gendcore version 4.5			P01519 conus geogr P32271 eubacterium P82177 shewarella
OM protein - protein search, using sw model				P81638 pyrococcus P80909 methanobact P50982 conus ermin
Run on:	May 8, 2001, 15:14:08 ; Search time 40.07 Seconds (without alignments)			P36207 ginkgo bilo P81755 conus texti P80612 zea mays (m
Title:	US-09-165-546A-11			P3391 Pseudomonas P28807 spinacia ol
Perfect score:	105			P32441 methanobact
Sequence:	1 GAASGLNGCRCRGARGPE 18			
Scoring table:	BLOSUM62			
	Gapop 10.0 , Gapext 0.5			
Searched:	93435 seqs, 3425486 residues			
Total number of hits satisfying chosen parameters:	1423			
Minimum DB seq length: 0				
Maximum DB seq length: 25				
Post-processing: Minimum Match 0%				
	Maximum Match 100%			
	Listing first 45 summaries			
Database :	SwissProt_39:*			
				Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
				SUMMARIES
Result No.	Score	Query Match	Length	DB ID Description
1	34.5	32.9	16	CXA1_CONEP
2	33.5	31.9	16	CXA1_CONPE
3	31	29.5	25	LYC_ASTRU
4	30	28.6	19	CXA2_CONST
5	29.5	28.1	15	CXA2_CONAL
6	28	27.1	12	CXA1_CONTM
7	28	26.7	25	MT_AGABI
8	27.5	26.2	16	CXA1_CONPE
9	27	26.2	25	MT_NEUCR
10	26	24.8	19	LCRP_PETWA
11	25	23.8	15	TAL_TREBR
12	25	23.8	17	FLAW_AZOCH
13	25	23.8	20	FLAW_AZOCV
14	24.5	23.3	22	INF_CICK
15	23.3	23	24	CXOA_CONSP
16	24	22.9	16	CXA1_CONAL
17	24	22.9	16	CXA2_CONMA
18	24	22.9	16	CXA3_CONAL
19	24	22.9	20	PSAF_PEA
20	24	22.9	23	CHIB_PEA
21	24	22.9	24	PSAC_CUCSA
22	24	22.9	25	CXA4_CONPU
23	24	22.9	25	CXOA_CONNA
24	24	22.9	25	G3P2_JACOR
25	24	22.9	25	K6P2_THEPH
26	24	22.9	25	LE01_BIOGL
27	23	21.9	13	CXA1_CONST
28	23	21.9	15	DIDH_PSEESP
29	23	21.9	22	LANM_STRMU
30	22	21.0	13	CXA2_CONGE
31	22	21.0	13	CXAA_CONST
32	22	21.0	14	CXA1_CONCN
33	22	21.0	14	CXA1_CONNMA
				RESULT 2
				CXA2_CONPE STANDARD
				ID CXAA_CONPE PRT; 16 AA.
				AC P50984; DT 01-OCT-1996 (Rel. 34, Created)
				DT 01-OCT-1996 (Rel. 34, Last sequence update)
				DE 30-MAY-2000 (Rel. 39, Last annotation update)
				DE ALPHA-CONOTOXIN PNIA.
				OS Conus pennaceus.
				OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
				OC Neogastropoda; Conoidea; Conidae; Conus.
				NCBI_TaxID=37335;
				OX

ALIGNMENTS

P01519 conus geogr
P32271 eubacterium
P82177 shewarella
P81638 pyrococcus
P80909 methanobact
P50982 conus ermin
P36207 ginkgo bilo
P81755 conus texti
P80612 zea mays (m
P3391 Pseudomonas
P28807 spinacia ol
P32441 methanobact

Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.

NCBI_TaxID=88764;

RN

X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).

RX

MEDLINE=98376423; PubMed=9708977;

RA

Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,

RA

Alewood P.F., Lewis R.J., Martin J.L.;

RT

"The 1.1-A resolution crystal structure of [Tyr15]EP1, a novel

alpha-conotoxin from Conus episopatus, solved by direct methods."

RL

Biochemistry 37:11425-11433(1998).

CC

-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY

CC

BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS

CC

INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC

CC

ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-

CC

3/BETA-4 SUBUNITS.

DR

PDB: 1A0M; 13-JAN-99.

KW

Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;

KW

Venom; Sulfatide; 3D-structure.

FT

DISULFID 2 8

FT

DISULFID 3 16

FT

SULFATION. 15 15

FT

MOD_RES 15 16

FT

MOD_AMIDATION. 16 16

SQ

SEQUENCE 16 AA; 1792 MW; C63385F376C99B4C CRC64;

Query Match 32.9%; Score 34.5%; DB 1; Length 16;

Best Local Similarity 42.9%; Pred. No. 46; Mismatches 4; Indels 3; Gaps 1;

Matches 6; Conservative 1;

Qy 8 GCC -- RCGARGPE 18

Db 1 GCCSDPRCMNNPD 14

[1] SEQUENCE.
 RN RP
 RP TISSUE=Venom;
 RX MEDLINE=94247719; PubMed=8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 Spira M.E., Zlotkin E.;
 RA "New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine receptors.";
 RT Biochemistry 33:9523-9529(1994).
 RL RN [2] SULFATATION OF TYR-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Wolfender F., Fainzilber M.,
 Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins alpha-PNA and alpha-PnIB: further investigation of labile sulfo- and phosphopeptides by electrospray, matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass spectrometry.";
 RT J. Mass Spectrom. 34:447-454(1999).
 RL RN [3] X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=96311277; PubMed=8740364;
 RA Hu S.-H., Gehrmann J., Guidat L.W., Alewood P.F., Craik D.J., Martin J.L.;
 RT "The 1.1 Å crystal structure of the neuronal acetylcholine receptor antagonist, alpha-conotoxin PnIA from Conus pennaceus.";
 RT Structure 4:417-423(1996).
 -: FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR), AND THUS INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
 DR IPEN; 21-APR-97.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Sulfatation; Venom; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match Score 33.5%; DB 1; Length 16;
 Best Local Similarity 42.9%; Pred. No. 63;
 Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 8 GCCR---CGARGPE 18
 ||| | | |;
 Db 1 GCCSLPPCAANNP 14

RESULT 3 LYC_ASTRU STANDARD; PRT; 25 AA.
 ID LYC_ASTRU
 AC P37715;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DE LYSOZYME (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE) (FRAGMENT).
 OS Asterias rubens (Common starfish).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa; Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Asterias.
 OC NCBI_TaxId=7604;
 RN [1] SEQUENCE.
 RX MEDLINE=75209004; PubMed=1149747;
 RA Jolles J., Jolles P.;
 RT "The lysozyme from Asterias rubens.";
 RL Eur. J. Biochem. 54:19-23(1975).
 -: CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES BETWEEN N-ACETYL-D-GLUCOSAMINE AND N-ACETYLGLURAMIC ACID IN PEPTIDOGLYCAN HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.

CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 DR PIR; A11762; A11762;
 DR InterPro; IPR001916;
 DR PROSITE; PS00128; LACTALBUMIN_LYSOCYME; PARTIAL.
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2568 MW; 6FA1D6BE87C5BE18 CRC64;

Query Match Score 29.5%; DB 1; Length 25;
 Best Local Similarity 41.2%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 7 NGCRC-----GARGP 17
 :||| | | | | | |
 Db 6 SGCLRCICVVEGSRMP 22

RESULT 4 CXA2_CONST STANDARD; PRT; 19 AA.
 ID CXA2_CONST
 AC P28879;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE ALPHA-CONOTOXIN STI (S2).
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 RN [1] RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Venom;
 RX MEDLINE=93003172; PubMed=1390774;
 RA Ramilo C., Zafaralla G.C., Nadasi L., Hammerland L.G., Yoshikami D., Gray W.R., Kristipati R., Ramchandran J., Miljanich G., Olivera B.M., Cruz L.J.;
 RA RT "Novel alpha- and omega-conotoxins from Conus striatus venom.";
 RL Biochemistry 31:3919-3926(1992).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANS, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR), AND THUS INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.
 DR IPEN; 21-APR-97.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Sulfatation; Venom; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match Score 30%; DB 1; Length 19;
 Best Local Similarity 60.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GCCRCGARGP 17
 ||| | | |
 Db 1 GCCCNPCAGP 10

RESULT 5 CXA2_CONAL STANDARD; PRT; 15 AA.
 ID CXA2_CONAL
 AC P56640;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ALPHA-CONOTOXIN AUTB.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 RN [1] RP SEQUENCE, AND SYNTHESIS.

- TISSUE=Venom; PubMed=97866965;
 RX MEDLINE=99003392; PubMed=97866965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin AuiB selectively blocks alpha3 beta4 nicotinic
 acetylcholine receptors and nicotine evoked norepinephrine release.";
 RT acetylcholine receptors and nicotine evoked norepinephrine release.";
 RL J. Neurosci. 18:8571-8579(1998).
 -: FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 ACETYLCOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC Post-synaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Venom.
 FT DISULFID 2 8
 FT DISULFID 3 15 AMIDATION
 MOD RES 15 15 MW: 84 EFE95FDC700155 CRC64;
 SEQUENCE 15 AA: 1578 MW;
- Query Match Score 29.5; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 2.e+02; Indels 3; Gaps 1;
 Matches 6; Conservative 1; Mismatches 4; Indels 3; Gaps 1;
- Qy 8 GCGR--CGARGP 18
 | | | | :
 Db 1 GCGSYPPCFATNFD 14
- RESULT 6
 CXA1_CONINM STANDARD; PRT; 12 AA.
 AC P56983;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ALPHA-CONOTOXIN IMI.
 OS Conus imperialis (Imperial cone).
 OC Eukaryota: Metazoa: Mollusca: Gastropoda: Caenogastropoda;
 NCBI_TaxID=35631; [1]
 RN SEQUENCE, AND SYNTHESIS.
 TISSUE=Venom; MEDLINE=94266889; PubMed=8206995;
 RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
 RA Gray W.R., Olivera B.M.;
 RT "A nicotinic acetylcholine receptor ligand of unique specificity,
 alpha-conotoxin IMI";
 RL J. Biol. Chem. 269:16733-16739(1994).
 RN CHARACTERIZATION.
 RX MEDLINE=95373776; PubMed=7651351;
 RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
 RA McIntosh J.M.;
 RT "Alpha-conotoxin IMI exhibits subtype-specific nicotinic
 acetylcholine receptor blockade: preferential inhibition of homomeric
 alpha 7 and alpha 9 receptors";
 RL Mol. Pharmacol. 48:194-199(1995).
 RN STRUCTURE BY NMR.
 RX MEDLINE=99212205; PubMed=10194298;
 RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
 RA Wunner D.E.;
 RT "NMR solution structure of alpha-conotoxin IMI and comparison to
 other conotoxins specific for neuronal nicotinic acetylcholine
 receptors";
 RL Biochemistry 38:3874-3882(1999).
 RN STRUCTURE BY NMR.
 RX MEDLINE=99158061; PubMed=10050774;
 RA Maslennikov I.V., Shenkarev Z.O., Zhunak M.N., Ivanov V.T.,
 RA Methfessel C., Tsetlin V.I., Arseniev A.S.;
- RT "NMR spatial structure of alpha-conotoxin IMI reveals a common
 scaffold in snail and snake toxins recognizing neuronal nicotinic
 acetylcholine receptors";
 RT STRUCTURE BY NMR.
 RL [5] RPN
 RP STRUCTURE BY NMR.
 RX MEDLINE=99324017; PubMed=10395477;
 RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
 RT "Solution structure of alpha-conotoxin IMI by 1H nuclear magnetic
 resonance";
 RL J. Med. Chem. 42:2364-2372(1999).
 -: FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
 RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
 WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGET NEURONAL
 NACHRS IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
 WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
 WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
 ALPHA-2/BETA-2, ALPHA-3/BETA-2, ALPHA-4/BETA-2, ALPHA-2/BETA-4,
 ALPHA-3/BETA-4, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
 CC PDB: 1IM1; 15-JUN-99.
 DR PDB: 1IM1; 15-JUN-99.
 DR PDB: 1CNL; 23-APR-99.
 DR PDB: 1CNL; 27-MAY-99.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Venom; 3D structure.
 FT DISULFID 3 12
 FT MOD_RES 12 12 AMIDATION.
 SQ 12 AA: 1357 MW; 9C29CE545A4176A CRC64;
- Query Match Score 27.1%; DB 1; Length 12;
 Best Local Similarity 54.5%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
- Qy 8 GCC---RCGAR 15
 | | | | :
 Db 1 GCGSDPRCAWR 11
- RESULT 7
 MT_AGABI STANDARD; PRT; 25 AA.
 ID MT_AGABI
 AC P04350;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-MAR-1987 (Rel. 35, Last sequence update)
 DE METALLOTHIONEIN (MT).
 OS Agaricus bisporus (Common mushroom).
 OC Eukaryota: Fungi; Basidiomycota; Hydnomycetes; Agaricales;
 OC Agaricaceae; Agaricus.
 OC NCBI_TAXID=5341; [1]
 RN SEQUENCE.
 RA STRAIN=A-32; TISSUE=Mycelium;
 RA Munger K., Larch K.;
 RT "Copper metallothionein from the fungus Agaricus bisporus: chemical
 and spectroscopic properties";
 RL Biochemistry 24:6751-6756(1985).
 CC -|- MISCELLANEOUS: THE SEVEN CYSTEINES BIND SIX COPPER (CUPROUS) IONS.
 CC -|- PROPERTIES OF THE COPPER MT ARE ATTRIBUTED TO THE METAL-THIOLEATE
 CC COMPLEX BECAUSE THEY ARE NOT PRESENT IN THE APOPROTEIN.
 CC -|- SIMILARITY: BELONGS TO FAMILY 8 IN METALLOTHIONEIN SUPERFAMILY.
 DR PIR: A03286; SWMR.
 KW Metal-binding Metal-thiolate cluster; Chelation; Copper.
 SQ 25 AA; 2233 MW; 33AB70F21023CF7 CRC64;
- Query Match Score 26.7%; DB 1; Length 25;
 Best Local Similarity 54.5%; Pred. No. 5.1e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	3	ASGLNGCCRCG 13	RESULT 8	CXAB_CONPNE	STANDARD;	PRT;	16 AA.
Db	14	ASGQCTSGCG 24	ID _CXAB_CONPNE				
AC	P50935;		AC	P50935;	Rel. 34, Created		
DT	01-OCT-1996	(Rel. 34, Created)	DT	01-OCT-1996	(Rel. 34, Last sequence update)		
DT	01-OCT-1996	(Rel. 34, Last sequence update)	DT	30-MAY-2000	(Rel. 39, Last annotation update)		
DE	ALPHA-CONOTOXIN PNIB.		DE	ALPHA-CONOTOXIN PNIB.			
OC	Conus pennaceus		OC	Conus pennaceus			
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;		OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomyctetes;			
OC	Neogastropoda; Conoidea; Conidae; Conus.		OC	Sordariales; Sordariaceae; Neurospora.			
NCBI_TaxID=37335;			NCBI_TaxID=5141;				
OX			OX				
RN	[1]	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.			
RP			RP				
RC			RC				
RX			RX				
TISSUE=Venom;			TISSUE=Venom;				
RA	Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D., Spira M.E., Zlotkin E.,		RA	Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D., Spira M.E., Zlotkin E.,			
RT	"New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine receptors."		RT	"New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine receptors."			
RL	Biochemistry 33:9523-9529(1994).		RL	Biochemistry 33:9523-9529(1994).			
RN	[2]		RN				
RP	SULFATATION OF TYR-15.		RP	SULFATATION OF TYR-15.			
RX	MEDLINE=93242956; PubMed=10226569;		RX	MEDLINE=93242956; PubMed=10226569;			
RA	Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M., Baldwin M.A., Burlingame A.L.,		RA	Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M., Baldwin M.A., Burlingame A.L.,			
RT	"Identification of tyrosine sulfation in Conus pennaceus conotoxins alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and phosphopeptides by electrospray matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass spectrometry."		RT	"Identification of tyrosine sulfation in Conus pennaceus conotoxins alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and phosphopeptides by electrospray matrix-assisted laser desorption/ionization (MALDI) and atmospheric pressure MALDI mass spectrometry."			
RT	J. Mass Spectrom. 34:447-454 (1999).		RT	J. Mass Spectrom. 34:447-454 (1999).			
RL	[3]		RL	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).		RP	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).			
RX	MEDLINE=97444322; PubMed=9298951;		RX	MEDLINE=97444322; PubMed=9298951;			
RU	Hu S.H., Gehrmann J., Alewood P.F., Craik D.J.J., Martin J.L.; RT		RU	Hu S.H., Gehrmann J., Alewood P.F., Craik D.J.J., Martin J.L.; RT			
RT	"Crystal structure at 1.1 Å resolution of alpha-conotoxin PnIB: comparison with alpha-conotoxins PnIA and GI."		RT	"Crystal structure at 1.1 Å resolution of alpha-conotoxin PnIB: comparison with alpha-conotoxins PnIA and GI."			
RL	Biochemistry 36:11323-11330(1997).		RL	Biochemistry 36:11323-11330(1997).			
CC	-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.		CC	-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSCS.			
CC	Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation; Sulfatation; venom; 3D-structure.		CC	Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation; Sulfatation; venom; 3D-structure.			
CC	KW		CC	KW			
CC	DISUFID 2 8		CC	DISUFID 2 8			
CC	DISUFID 3 16		CC	DISUFID 3 16			
CC	MOD_RES 15 15		CC	MOD_RES 15 15			
CC	MOD_RES 16 16		CC	MOD_RES 16 16			
CC	SEQUENCE 16 AA; 1643 MW;		CC	SEQUENCE 16 AA; 1643 MW;			
CC	CRC64;		CC	CRC64;			
DR	X03009; CAA2793.1;		DR	X03009; CAA2793.1;			
DR	EMBL; M59836; AAA33594.1;		DR	EMBL; M59836; AAA33594.1;			
DR	M2709; AAA33595.1;		DR	M2709; AAA33595.1;			
KW	Metal-thiolate cluster; Chelation; Copper.		KW	Metal-thiolate cluster; Chelation; Copper.			
FT	INIT_MET 0 0		FT	INIT_MET 0 0			
FT	METAL 3 3		FT	METAL 3 3			
FT	METAL 5 5		FT	METAL 5 5			
FT	METAL 11 11		FT	METAL 11 11			
FT	METAL 13 13		FT	METAL 13 13			
FT	METAL 17 17		FT	METAL 17 17			
FT	METAL 19 19		FT	METAL 19 19			
FT	METAL 22 22		FT	METAL 22 22			
FT	CONFFLICT 21 21		FT	CONFFLICT 21 21			
FT	N -> T (IN REF. 2)		FT	N -> T (IN REF. 2)			
FT	SEQUENCE 25 AA.		FT	SEQUENCE 25 AA.			

	Query Match Best Local Similarity Matches	Score 26.2%; 41.7%; 5; Conservative	Length 25; Pred. No. 5.9e+02;	DB 1; Indels	Length 25;	Score 27.5; Pred. No. 5.9e+02;	DB 1; Indels	Length 25;	Score 23.8%; 66.7%; 6; Conservative	DB 1; Indels	Length 15; Pred. No. 8.9e+02;	Score 25; 66.7%; 1; Mismatches 0;	DB 1; Indels	Length 15;	Score 23.8%; 50.0%; 3; Mismatches 1;	DB 1; Indels	Length 15;	Score 25; 50.0%; 1; Mismatches 0;	DB 1; Indels	Length 15;	Score 23.8%; 50.0%; 3; Mismatches 1;	DB 1; Indels	Length 15;		
Qy	8 GC-----CRCGA 14																								
Db	4 GCGSASSCNGS 15																								
RESULT 10																									
LCRP_PETMVA	ID LCRP_PETMVA	STANDARD;	PRT;	19 AA.																					
AC	Q10986;																								
DT	01-OCT-1996 (Rel. 34; Created)																								
DT	01-OCT-1996 (Rel. 34; Last sequence update)																								
DT	15-JUL-1998 (Rel. 36; Last annotation update)																								
DE	CORTICOSTATIN RELATED PROTEIN LCRP.																								
OS	Petromyzon marinus (Sea Lamprey).																								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzoniformes; Petromyzontidae; Petromyzon.																								
OC	NCBL_TaxID=7757;																								
RN	[1]																								
RP	SEQUENCE.																								
RX	MEDLINE=96321324; PubMed=8759287;																								
RA	Conlon J.M., Sower S.A.;																								
RA	"Isolation of a peptide structurally related to mammalian corticotropins from the lamprey Petromyzon marinus.";																								
RA	Comp. Biochem. Physiol. 114B:133-137 (1996).																								
CC	- - FUNCTION: MAY HAVE MICROCIDAL ACTIVITIES. MAY INHIBIT CORTICOTROPIN (ACTH) STIMULATED STEROIDOGENESIS AND THE MICROBIAL ACTIONS OF THE CORTICOSTATINS.																								
CC	- - MASS SPECTROMETRY: MW=2201; MW ER=0.4; METID=ELCTROPRAY.																								
CC	- - SIMILARITY: BELONGS TO THE FAMILY OF CORTICOSTATIN/DEFENSIN PEPTIDES.																								
KW	Defensin; Antibiotic.																								
FT	DISULFID 1 18 BY SIMILARITY.																								
FT	DISULFID 3 9 BY SIMILARITY.																								
FT	DISULFID 8 17 BY SIMILARITY.																								
FT	DISULFID 8 17 BY SIMILARITY.																								
SQ	SEQUENCE 19 AA; 2209 MW; 8D9CEDC71A199AE5 CRC64;																								
Query Match Best Local Similarity Matches	4; Conservative	Score 26;	DB 1;	Length 19;	0; Mismatches 2;	Indels 0;	Gaps 0;																		
Qy	10 CRCGAR 15																								
Db	1 CPCGRR 6																								
RESULT 11																									
TAI_TREBRR	ID TAI_TREBRR	STANDARD;	PRT;	15 AA.																					
AC	P34070;																								
DT	01-FEB-1994 (Rel. 28; Created)																								
DT	01-FEB-1994 (Rel. 28; Last sequence update)																								
DE	TREMEROGEN A-I.																								
OC	Tremella brasiliensis (Jelly fungus).																								
OC	Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Tremellales; Tremellaceae; Tremella.																								
OC	NCBI_TaxID=298996;																								
RN	[1]																								
RP	SEQUENCE.																								
RT	Ishibashi Y., Sakagami Y., Isogai A., Suzuki A.; Peptidyl sex hormones of Tremellosporous A-9291-I and A-9291-VIII.																								
RT	Biochemistry 23:1389-1404 (1984).																								
-I- FUNCTION: TREMEROGEN A-I IS PRODUCED BY THE A MATING-TYPE CELLS AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.																									
CC	Pheromone: Prenylation; Lipoprotein.																								
CC	Sequence: "Structures of Tremellosporous A-9291-I and A-9291-VIII."																								
RT	-I- FUNCTION: TREMEROGEN A-I IS PRODUCED BY THE A MATING-TYPE CELLS AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.																								
CC	Pheromone: Prenylation; Lipoprotein.																								
RT	SEQUENCE.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-I.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-VIII.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-VII.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-VI.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-IV.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-III.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-II.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-I.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-IV.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-III.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-II.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-I.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-IV.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-III.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-II.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-I.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-IV.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-III.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-II.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-I.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-IV.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-III.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-II.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-I.																								
RT	STRUCTURE OF TREMELLOSPOROUS A-9291-V.																								

"Flavodoxin 1 of Azotobacter vinelandii: characterization and role in electron donation to purified assimilatory nitrate reductase.";
 RL Biochem. J. 317:103-108 (1996).
 -I- FUNCTION: LOW-POTENTIAL ELECTRON DONOR TO A NUMBER OF REDOX ENZYMES.
 CC -I- COFACTOR: FMN
 CC -I- SUBUNIT: MONOMER.
 CC -I- MASS SPECTROMETRY: MW=19430; MW.ERR=3; METHOD=ELECTROSPRAY.
 CC -I- SIMILARITY: BELONGS TO THE FLAVODOXIN FAMILY.
 DR InterPro; IPR001226;
 DR Pfam; PF00288; flavodoxin_1;
 DR PROSITE; PS00201; FLAVODOXIN; PARTIAL.
 KW Electron transport; Flavoprotein; FMN.
 FT NON-TER 20
 SEQUENCE 20 AA; 2043 MW; 95B3601FAD7D4A36 CRC64;

Query Match Score 25; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAASGLNG 8
 1::1: 1
 Db 8 GSSSGVTC 15

RESULT 14
 ID ANFC_CHICK STANDARD; PRT; 22 AA.
 AC P21805;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE C-TYPE Natriuretic Peptide (CNP).
 GN NPc.
 OS Gallus gallus (Chicken).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN NCBI_TaxID=9031;
 [1]
 RP SEQUENCE.
 RC TISSUE-Brain;
 RX MEDLINE=91113186; PubMed=1989595;
 RA Arimura J.J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation and identification of C-type natriuretic peptide in chicken brain."
 RL Biochem. Biophys. Res. Commun. 174:142-148 (1991).
 CC -I- FUNCTION: VASORELAXANT ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
 CC -I- SUBCELLULAR LOCATION: SECRETED.
 CC -I- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 DR PIR; JT0581; JT0581;
 DR InterPro; IPR000663; -.
 DR Pfam; PF00212; ANP; 1.
 DR PRINTS; PR00710; NATPEPTIDES.
 DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
 KW Vasoactive.

FT DISULFID 6 22 AA; 2244 MW; FC2A4706D8DAC025 CRC64;

AC P28800;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE OMEGA-CONOTOXIN SVIA.
 OS Conus striatus (Striated cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6493;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE-Venom;
 RX MEDLINE=93003172; PubMed=139074;
 RA Ramallo C., Zafaralla G.C., Nadasaki L., Hammerland L.G., Yoshikami D., Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M., Cruz L.J.;
 RA "Novel alpha- and omega-conotoxins from Conus striatus venom.";
 RL Biochemistry 31:9919-9926 (1992).
 CC -I- FUNCTION: OMEGA-CONOTOXINS ACT AT PRESYNAPTIC MEMBRANES, THEY BIND AND BLOCK THE CALCIUM CHANNELS.
 DR PIR; B44379; B44379.
 KW Presynaptic neurotoxin; Calcium channel inhibitor; Venon;
 KW Amicidin; Hydroxylation; Calcium channel inhibitor; Venon;
 FT DISULFID 1 15
 FT DISULFID 8 18
 FT DISULFID 14 23
 FT MOD_RES 7 7 HYDROXYLATION.
 SQ SEQUENCE 24 AA; 2485 MW; B29EFC982ABBE644 CRC64;

Query Match Score 24.5; DB 1; Length 24;
 Best Local Similarity 38.5%; Pred. No. 1.5e+03;
 Matches 5; conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 GAASGLNGCRCG 13
 1: 1: 1 1 1
 Db 5 GSPGCVTSC-CG 16

Search completed: May 8, 2001, 15:14:08
 Job time: 529 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:16:06 ; Search time 114.89 Seconds

(without alignments)
18.363 Million cell updates/sec

Title: US-09-165-546A-11
Perfect score: 105

Sequence: 1 GAASGLNCCRCGARGPE 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374/700 seqs, 117/207/15 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 10%
Maximum Match 10%

Listing first 45 summaries

SPTREMBL_15; *

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

ALIGNMENTS

	RESULT	1
ID	Q17072	PRELIMINARY;
AC	Q17072;	PRT;
DT	01-NOV-1996	(TREMBLrel. 01, Created)
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)
DE	SILKMOTH CHORION mRNA (FRAGMENT).	
OS	Antheraea polyphemus (Polyphemus moth).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptrysia;	
OB	Bombycoidea; Saturniidae; Saturniinae; Antherea.	
[1]	NCBI_TaxID=7120;	
RN		
RP		
SEQUENCE FROM N.A.		
RX		
MEDLINE=8237860; PubMed=277327;		
RA		
Sim G.K., Efstratiadis A., Jones C.W., Kafatos F.C., Koehler M.,		
Kronenberg H.M., Maniatis T., Regier J.C., Roberts B.F., Rosenthal N.;		
RA		
RT		"Studies on the structure of genes expressed during development."
RL		Cold Spring Harb. Symp. Quant. Biol. 42:333-945(1978).
DR		
EMBL: M10845; AAA27784.1; -.		
KW		
Chorion.		
FT		
NON_TER	1	1
FT	22	22
NON_TER	1	1
SEQUENCE	22 AA;	1944 MW;
		14AD250B918DD680D CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Query	Match	Length	DB	ID	Description
1	36.5	34.8	22	5	Q17072	017072 antheraea P
2	34	32.4	18	11	063136	063136 rattus norv
3	30.5	29.0	24	3	000059	000059 uromyces fa
4	29.5	28.1	16	5	P82706	P82706 drosophila
5	29.5	28.1	18	4	Q14042	Q14042 homo sapien
6	28	26.7	18	13	Q90790	Q90790 gallus galli
7	27.5	26.2	25	4	Q9wW14	Q9wW14 pseudomonas
8	27	25.7	24	6	Q28787	Q28787 papiro sp. (
9	27	25.7	24	6	Q28430	Q28430 gorilla gor
10	27	25.7	24	6	Q28781	Q28781 pongo pygma
11	26	24.8	24	11	089021	089021 mus musculus
12	25	23.8	13	4	P82276	P82276 homo sapien
13	25	23.8	18	4	Q9DE38	Q9DE38 homo sapien
14	25	23.8	19	2	Q9S1W0	Q9S1W0 streptomyce
15	25	23.8	21	4	Q07101	Q07101 homo sapien
16	25	23.8	21	4	Q9DN06	Q9DN06 homo sapien
17	25	23.8	21	5	Q9u400	Q9u400 drosophila
18	25	23.8	24	5	P82176	P82176 gallera me
19	24	22.9	9	5	Q9tWD6	Q9tWD6 leptinotars

RESULT 2

Qy	5 GLNGC-CRCG 13
ID	Q63136
PRT;	18 AA.
AC	Q63136;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)	Qy	6	LNGC---CRCGA 14
DE	RAT ALPHA-CRYSTALLIN B CHAIN.		Db	1	: _ _
OS	Rattus norvegicus (Rat).				MNPCCSSNNSCGA 12
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.				
NCBI_TaxID=10116;					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	Medline=91093055; PubMed=2176207;				
RA	Iwaki A., Iwaki T., Goldman J. E., Liem R.K.;				
RT	"Multiple mRNAs of rat brain alpha-crystallin B chain result from alternative transcriptional initiation.";				
RT	J. Biol. Chem. 265:22197-22203(1990).				
RL	EMBL: M55234; AAA40974.1; -				
DR	SEQUENCE 18 AA; 1963 MW;				
SQ	1D4F384151EF1DDB CRC64;				
RESULT	4				
PB2706		PRELIMINARY;	PRT;	16	AA.
ID	PB2706				
AC	PB2706;				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)				
DE	IMMUNE-INDUCED PROTEIN 1 (DIN-1)				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriodea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=OREGON-R; TISSUE=HEMOLYMPH;				
RX	MEDLINE=98409659; PubMed=9746738;				
RA	Uittenblijler-Joseph S., Moniatte M., Lagueux M., Van Dorsselaer A.,				
RA	Hoffmann J.A., Bulet P.;				
RT	"Different display of peptides induced during the immune response of Drosophila: a matrix-assisted laser desorption ionization time-of-flight mass spectrometry study.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 95:11342-11347(1998).				
RL	CC				
- -	TISSUE SPECIFICITY: HEMOLYMPH.				
CC	- - INDUCTION: BY BACTERIAL INFECTIOIN.				
CC	- - MASS SPECTROMETRY: MW=1687.7; METHOD=MALDI.				
KW	Antibiotic; Insect immunity; Amidation.				
FT	MOD-RES 16				
FT	DISULFID 9				
FT	SEQUENCE 16 AA; 1670 MW;				
SQ	5F22356839CD06AF CRC64;				
Query Match		28.1%			
Best Local Similarity		Score 29.5;	DB 5;	Length 16;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	4;	Mismatches 1;	Gaps 1;		
Query Match		28.1%			
Best Local Similarity		Score 29.5;	DB 5;	Length 16;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	4;	Mismatches 1;	Gaps 1;		
Query Match		28.1%			
Best Local Similarity		Score 29.5;	DB 5;	Length 16;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	4;	Mismatches 1;	Gaps 1;		
RESULT	5				
Q14042		PRELIMINARY;	PRT;	18	AA.
ID	Q14042				
AC	Q14042;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DE	TYPE II PROCOLLAGEN (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OC	NCBI_TaxID=9606;				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
CC	INTERPRO; PS00203; MTALLOTHIONINE_VRT; 1.				
CC	Metal-binding; Copper; Chelation.				
CC	METAL 4 COPPER (BY SIMILARITY).				
CC	METAL 8 COPPER (BY SIMILARITY).				
CC	METAL 10 COPPER (BY SIMILARITY).				
CC	METAL 14 COPPER (BY SIMILARITY).				
CC	METAL 16 COPPER (BY SIMILARITY).				
CC	METAL 19 COPPER (BY SIMILARITY).				
DR	INTERPRO; IPR00006; -				
DR	Metal-thionein.				
KW	METALLOTHIONINE.				
FT	METAL 4 COPPER (BY SIMILARITY).				
FT	METAL 8 COPPER (BY SIMILARITY).				
FT	METAL 10 COPPER (BY SIMILARITY).				
FT	METAL 14 COPPER (BY SIMILARITY).				
FT	METAL 16 COPPER (BY SIMILARITY).				
FT	METAL 19 COPPER (BY SIMILARITY).				
SQ	SEQUENCE 24 AA; 2383 MW;				
	563C42F3CB8A6F60E CRC64;				
Query Match		28.1%			
Best Local Similarity		Score 29.5;	DB 4;	Length 18;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	7;	Mismatches 1;	Gaps 1;		
Query Match		29.0%			
Best Local Similarity		Score 30.5;	DB 3;	Length 24;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	2;	Mismatches 1;	Gaps 1;		
Query Match		29.0%			
Best Local Similarity		Score 30.5;	DB 3;	Length 24;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	2;	Mismatches 1;	Gaps 1;		
Query Match		29.0%			
Best Local Similarity		Score 30.5;	DB 3;	Length 24;	
Matches		50.0%;	Pred. No. 5.4e+02;		
Indels	2;	Mismatches 1;	Gaps 1;		

RESULT	6						
Q97790	PRELIMINARY;	PRT;	18 AA.				
ID Q97790;							
AC 097790;							
DT 01-NOV-1996 (TREMBLrel. 01, Created)							
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)							
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)							
DE ALPHA-1 TYPE III COLLAGEN (FRAGMENT).							
OS Gallus gallus (Chicken).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Gallus.							
OC NCBI_TaxID=9031;							
OX [1]							
RP SEQUENCE FROM N.A.							
RX MEDLINE-#8135706; PubMed=6298201;							
RA Yamada Y., Mudryj M., Sullivan M., de Crombrugghe B.;							
RT "Isolation and characterization of a genomic clone encoding chick alpha 1 type III collagen".							
RT J. Biol. Chem. 258:2758-2761.(1983).							
DR EMBL: Y00391; CAA23689.1; -.							
SQ SEQUENCE 18 AA; 1732 MW; 439C34D5A9329EBC CRC64;							
Query Match	26.7%	Score 28;	DB 13;	Length 18;			
Best Local Similarity	100.0%	Pred. No. 9.8e+0;	Indels 0;	Gaps 0;			
Matches 5; Conservative	0;	Mismatches 0;					
Qy 13 GARGP 17							
Db 7 GARGP 11							
RESULT	7						
Q9WW14	PRELIMINARY;	PRT;	25 AA.				
ID Q9WW14							
AC Q9WW14;							
DT 01-NOV-1999 (TREMBLrel. 12, Created)							
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)							
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)							
DE GDP-MANNOSE DEHYDROGENASE (FRAGMENT).							
GN ALGD.							
OS Pseudomonas syringae (pv. syringae).							
OC Pseudomonas; Proteobacteria; gamma subdivision; Pseudomonadaceae;							
OC Pseudomonas.							
OX NCBI_TaxID=321;							
RP SEQUENCE FROM N.A.							
RC STRAIN=SF5;							
RX MEDLINE-#9287831; PubMed=10348861;							
RA Fakhr M.K., Penalosa-Vazquez A.M., Bender C.L.,							
RT "Regulation of alginate biosynthesis in <i>Pseudomonas syringae</i> pv. syringae."							
RT J. Bacteriol. 181:3478-3485(1999).							
DR EMBL: AF131068; ADD31821.1; -.							
FT NON_TER 25	25						
SQ SEQUENCE 25 AA; 2531 MW; DE2F6B5D4D19EICA CRC64;							
Query Match	26.2%	Score 27.5;	DB 2;	Length 25;			
Best Local Similarity	71.4%	Pred. No. 1.5e+03;	Indels 1;	Gaps 1;			
Matches 5; Conservative	0;	Mismatches 1;					
Qy 8 GC-CRCG 13							
Db 17 GCUCACG 23							
RESULT	8						
Q28787	PRELIMINARY;	PRT;	24 AA.				
ID Q28787							
RP SEQUENCE FROM N.A.							
RC STRAIN=BABA;							
RA Evans B.B.A., Fu P., Tregear G.G.W.;							
RL J. Mol. Endocrinol. 0:0-0(1993).							
CC - - SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).							
CC - - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.							
CC NCBI_TaxID=61183;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=RG YK;							
RA Evans B.B.A., Fu P., Tregear G.G.W.;							
RL J. Mol. Endocrinol. 0:0-0(1993).							
CC - - FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE INVOLVED IN REMODELLING OF CONNECTIVE TISSUES DURING PREGNANCY, PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.							
CC - - SUBUNIT: HETERO DIAMER OF A CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).							
CC - - SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).							
CC - - TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY AND IN THE PLACENTA (BY SIMILARITY).							
CC - - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.							
CC NCBI_TaxID=9595;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=RG YK;							
RA Evans B.B.A., Fu P., Tregear G.G.W.;							
RL J. Mol. Endocrinol. 0:0-0(1993).							
CC - - FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE INVOLVED IN REMODELLING OF CONNECTIVE TISSUES DURING PREGNANCY, PROMOTING GROWTH OF PUBIC LIGAMENTS AND RIPENING OF THE CERVIX.							
CC - - SUBUNIT: HETERO DIAMER OF A CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY).							
CC - - SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).							
CC - - TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LUTEUM OF PREGNANCY AND IN THE PLACENTA (BY SIMILARITY).							
CC - - SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.							
CC NCBI_TaxID=22728;							
RN [1]							
RP SEQUENCE FROM N.A.							
RC STRAIN=SF5;							
RX MEDLINE-#9287831; PubMed=10348861;							
RA Fakhr M.K., Penalosa-Vazquez A.M., Bender C.L.,							
RT "Regulation of alginate biosynthesis in <i>Pseudomonas syringae</i> pv. syringae."							
RT J. Bacteriol. 181:3478-3485(1999).							
DR EMBL: AF131068; ADD31821.1; -.							
FT NON_TER 25	25						
SQ SEQUENCE 25 AA; 2531 MW; DE2F6B5D4D19EICA CRC64;							
Query Match	25.7%	Score 27;	DB 6;	Length 24;			
Best Local Similarity	70.0%	Pred. No. 1.5e+03;	Indels 0;	Gaps 0;			
Matches 5; Conservative	0;	Mismatches 0;					
Qy 1 ID Q28787							

Best Local Similarity 57.1%; Pred. No. 1.7e+03; Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	SQ	SEQUENCE	24 AA;	2502 MW;	BIABBA4650DC0BFP4 CRC64;
Qy 7 NGCRG 13 ID 089021; AC 028781; DT 01-NOV-1996 (TREMBLrel. 01, Created) DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update) DE RELAXIN 1B (FRAGMENT). GN RLX 1B. OS Pongo pygmaeus (Orangutan). OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo. OX NCBI_TaxID=9600; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=RG YK 287; RA Evans B.B.A., Fu P., Tregebar G.G.W.; RL J. Mol. Endocrinol. 0;0-0(1993). CC -!- FUNCTION: RELAXIN IS AN OVARIAN HORMONE THAT ACTS WITH ESTROGEN TO PRODUCE DILATATION OF THE BIRTH CANAL IN MANY MAMMALS. MAY BE INVOLVED IN REMODELLING OF CONNECTIVE TISSUES DURING PREGNANCY, PROMOTING GROWTH OF PUBLIC LIGAMENTS AND RIPENING OF THE CERVIX. CC -!- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO DISULFIDE BONDS (BY SIMILARITY). CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE CORPUS LOUTEUM OF PREGNANCY AND IN THE PLACENTA (BY SIMILARITY). CC -!- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY. DR EMBL: 227229; CAA81743; 1. . DR INTERPRO: IPR000739; . DR PROSTIE; PS00267; INSULIN; 1. KW Insulin family; Hormone; Multigene family; Polymorphism. FT NON_TER 1 SQ SEQUENCE 24 AA; 2673 MW; 5615D4B92C1DFD24 CRC64;	Query Match Score 26; DB 11; Length 24; Best Local Similarity 45.5%; Pred. No. 2.4e+03; Matches 5; Conservative 4; Indels 0; Gaps 0;	Qy 1 GAASGLNGCCR 11 ID 089021; AC 028781; DT 01-NOV-1996 (TREMBLrel. 08, Created) DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update) DE MUSCULAR CHLORIDE CHANNEL 1 (FRAGMENT). GN CLC1. OS Mus musculus (Mouse). OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Vulnifor D.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. OX NCBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=BALB/C; TISSUE=SKELETAL MUSCLE; RA Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. DR EMBL; AJ011106; CAA09489.1; -. FT NON_TER 1	Query Match Score 26; DB 11; Length 24; Best Local Similarity 45.5%; Pred. No. 2.4e+03; Matches 5; Conservative 4; Indels 0; Gaps 0;		
RESULT 10 Q28781 PRELIMINARY; PRT; 24 AA.	RESULT 12 P82276 PRELIMINARY; ID P82276 AC PB2276; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DE TUBULIN ASSOCIATED PEPTIDE (FRAGMENT). OS Homo sapiens (Human). OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9600; RN [1] RP SEQUENCE. RA Rossbacher J., Gartner W., Katinger H., Wagner L.; RT Haemoglobin mediated changes in cellular immune response. ; RL Submitted (JAN-2000) to the SWISS-PROT data bank. CC -!- TISSUE SPECIFICITY: LEUKOCYTES AND HEPATOCYTES. KW Microtubules. FT NON_TER 1 FT NON_TER 13 SQ SEQUENCE 13 AA; 1300 MW; 4FD05B1E478D6227 CRC64;	Query Match Score 25; DB 4; Length 13; Best Local Similarity 85.7%; Pred. No. 2e+03; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
RESULT 11 Q28781 PRELIMINARY; PRT; 24 AA.	RESULT 13 Q9UE38 PRELIMINARY; ID Q9UE38 AC Q9UE38; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DE COLLAGEN. OS Homo sapiens (Human). OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9600; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE-89325561; PubMed=2753125; RA Viikula M., Peitonen L.; "Structural analyses of the polymorphic area in type II collagen gene." FEBS Lett. 230:171-174 (1989). DR DR KW Collagen. SQ SEQUENCE 18 AA; 1683 MW; 7724306D60CA21B4 CRC64;	Query Match Score 25; DB 4; Length 18; Best Local Similarity 66.7%; Pred. No. 2.7e+03; Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			

QY 13 GARGPE 18
| :|||
Db 4 GEGPPE 9

RESULT 14
Q9SIW0 PRELIMINARY; PRT; 19 AA.
ID Q9SIW0;
AC (TREMBUREL. 13, Created)
DT 01-MAY-2000 (TREMBUREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMBUREL. 13, Last annotation update)
DE SMALL HYPOTHETICAL PROTEIN.
GN SCU4.13C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TAXID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapaitre D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
EMBL; ALL09930; CAB52947.1;
SQ SEQUENCE 19 AA; 2028 MW; F643A294D0127DF6 CRC64;

Query Match 23.8%; Score 25; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 GCCRC 12
Db 12 GACQC 16

RESULT 15
Q07101 PRELIMINARY; PRT; 21 AA.
ID Q07101;
AC (TREMBUREL. 01, Created)
DT 01-NOV-1996 (TREMBUREL. 01, Last sequence update)
DT 01-NOV-1998 (TREMBUREL. 08, Last annotation update)
DE PLACENTAL GROWTH FACTOR 2 (PLGF-2) (FRAGMENT).
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=93205407; PubMed=7681160;
RA Maglione D., Guerriero V., Viglietto G., Ferraro M.G., Appelikova O.,
Alitalo K., del Vecchio S., Lei K.J., Chou J.Y., Persico M.G.;
RT "Two alternative mRNAs coding for the angiogenic factor, Placenta
growth factor (PLGF), are transcribed from a single gene of chromosome
14.";
RL Oncogene 8:925-931(1993);
DR EMBL; SS7152; AAB25832.1; -.
KW Growth factor; Placenta.

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I protein - protein search, using sw model

Search on: May 8, 2001, 15:07:10 ; Search time 113.31 Seconds
 (without alignments)
 9.081 Million cell updates/sec

title: US-09-165-546A-12

perfect score: 91

sequence: 1 SRLLEFYLAMPFATPMEA 18

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 165078

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : A_Geneseq_0401:*

1:	/SIDS6/gcdata/geneseq/geneseq/AA1980.DAT:*
2:	/SIDS6/gcdata/geneseq/geneseq/AA1981.DAT:*
3:	/SIDS6/gcdata/geneseq/geneseq/AA1982.DAT:*
4:	/SIDS6/gcdata/geneseq/geneseq/AA1983.DAT:*
5:	/SIDS6/gcdata/geneseq/geneseq/AA1984.DAT:*
6:	/SIDS6/gcdata/geneseq/geneseq/AA1985.DAT:*
7:	/SIDS6/gcdata/geneseq/geneseq/AA1986.DAT:*
8:	/SIDS6/gcdata/geneseq/geneseq/AA1987.DAT:*
9:	/SIDS6/gcdata/geneseq/geneseq/AA1988.DAT:*
10:	/SIDS6/gcdata/geneseq/geneseq/AA1989.DAT:*
11:	/SIDS6/gcdata/geneseq/geneseq/AA1990.DAT:*
12:	/SIDS6/gcdata/geneseq/geneseq/AA1991.DAT:*
13:	/SIDS6/gcdata/geneseq/geneseq/AA1992.DAT:*
14:	/SIDS6/gcdata/geneseq/geneseq/AA1993.DAT:*
15:	/SIDS6/gcdata/geneseq/geneseq/AA1994.DAT:*
16:	/SIDS6/gcdata/geneseq/geneseq/AA1995.DAT:*
17:	/SIDS6/gcdata/geneseq/geneseq/AA1996.DAT:*
18:	/SIDS6/gcdata/geneseq/geneseq/AA1997.DAT:*
19:	/SIDS6/gcdata/geneseq/geneseq/AA1998.DAT:*
20:	/SIDS6/gcdata/geneseq/geneseq/AA1999.DAT:*
21:	/SIDS6/gcdata/geneseq/geneseq/AA2000.DAT:*
22:	/SIDS6/gcdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Suit No.	Score	Query	Match	Length	DB	ID	Description
1	91	100 0	18	21	Y52439		Human tumour anti
2	54	59.3	10	20	Y06013		Human cancer anti
3	52	57.1	10	20	Y06004		Human cancer anti
4	52	57.1	10	20	Y06007		Human cancer anti
5	51	56.0	10	20	Y06010		Human cancer anti
6	44	48.4	9	21	Y06021		NY-ESO-1 derived H
7	44	48.4	9	21	Y78465		Protein kinase P65
8	37	40.7	11	21	B12647		Human MAP kinase S
9	37	40.7	15	21	Y66184		Human MAP kinase S
10	37	40.7	15	21	Y66185		Human MAP kinase S
11	37	40.7	15	21	Y66509		Human MAP kinase S

Human MAP kinase S									
15	21	Y66510							
13	39.6	9	21	Y79757					
14	35.2	17	15	R49308					
15	34.1	16	18	W10317					
16	33.0	9	21	Y79752					
17	33.0	10	20	Y06056					
18	33.0	10	20	Y05990					
19	33.0	12	18	W16119					
20	33.0	12	19	W68759					
21	33.0	12	19	W58246					
22	33.0	12	20	Y09890					
23	33.0	12	21	B17671					
24	33.0	14	14	R36921					
25	33.0	24	19	W68467					
26	29	31.9	14	W59119					
27	29	31.9	19	W68469					
28	29	31.9	24	Y27475					
29	28	30.8	10	W16102					
30	28	30.8	10	W68740					
31	28	30.8	10	W58219					
32	28	30.8	10	Y09869					
33	28	30.8	10	B17654					
34	28	30.8	14	Y45370					
35	28	30.8	21	W88700					
36	27	29.7	9	Y82843					
37	27	29.7	10	W16201					
38	27	29.7	10	W16023					
39	27	29.7	10	W68661					
40	27	29.7	10	W68819					
41	27	29.7	10	W58140					
42	27	29.7	10	W58327					
43	27	29.7	10	Y09971					
44	27	29.7	10	Y09784					
45	27	29.7	10	B17588					

ALIGNMENT S

RESULT 1
 Y52439 Human tumour antigen NY-ESO-1 peptide #12.
 ID Y52439 standard; Protein: 18 AA.
 XX
 AC Y52439;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Human tumour antigen NY-ESO-1 peptide #12.
 XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
 KW T-cell; helper; stimulation; proliferation; treatment;
 KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
 KW prognosis; hepatoma; thyroid cancer; bladder cancer; lung cancer;
 KW lymphoma.

is derived by analysis of the total score distribution.

US Homo sapiens.
 XX WO9953938-A1.
 PN XX
 PD XX 28-OCT-1999.
 XX PF 24-MAR-1999; 99WO-US06875.
 XX PR 17-APR-1998; 98US-0062422.
 PR 02-OCT-1998; 98US-0165546.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Stockert E, Jager E,
 PI Gure A, Ritter G;
 XX DR WPI: 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes

XX Claim 4; Page 22; 49pp; English.

XX Peptides #8-#13 (Y52435-Y52440) which can bind to MHC major
 CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
 CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
 CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels
 CC in normal ovary and testis, but not in normal colon, kidney, liver,
 CC brain, oesophagus and skin.
 CC It was expressed in certain tumours and
 CC tumour cell lines with some degree of frequency - these included
 CC melanoma specimens and cell lines, and breast and bladder cancer
 CC specimens, with expression in other tumour types being sporadic.
 CC These NY-ESO-1-derived peptides may be used in methods and
 CC compositions used for the treatment, diagnosis and prevention of
 CC cancers (such as melanoma, breast cancer, prostate cancer, lung
 CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
 CC or lymphoma) and to stimulate the proliferation of T cells.

XX Sequence 18 AA;

Query Match 100.0%; Score 91; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 18 AA;

Query Match 59.3%; Score 54; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

RESULT 2
 Y06013 standard; Peptide; 10 AA.
 XX

XX AC Y06013;

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.
 XX Homo sapiens.

XX OS WO9918206-A2.

XX PD 15-APR-1999.

XX PP 21-SEP-1998; 98WO-US19609.

XX PI Rosenberg SA, Wang RF;

XX DR WPI: 1999-277270/23.

XX PR 08-OCT-1997; 97US-0061428.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PS Example 10; Page 42; 88pp; English.

XX PI Rosenberg SA, Wang RF;

XX DR WPI: 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3

XX PT Example 10; Page 42; 88pp; English.

XX PS Example 10; Page 42; 88pp; English.

CC This peptide was identified as an HLA peptide motif following a
 CC screen for epitopes from the coding region of human ESO-1/CAG-3
 CC ORF1 (see X58599). 30 Epitopes (see Y05988-Y06017) were identified.
 CC The present peptide (ranked 26) corresponds to amino acid residues
 CC 91-100 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent
 CC tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides (see Y05967-87) derived from
 CC CAG-3, portions of CAG-3 and their variants, are useful as cancer
 CC vaccines. A claimed method of preventing or inhibiting cancer
 CC involves administering a cancer peptide, with or without an HLA
 CC molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.

XX Sequence 10 AA;

Query Match 59.3%; Score 54; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

Query Match 7 YLAMPFATM 16
 Best Local Similarity 100.0%; Pred. No. 0.0036;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 10 AA;

response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

Sequence 10 AA;

Query Match 57.1%; Score 52; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Indels 0; Gaps 0;

Query 3 LLFFYLAMPF 12
|||||||
Db 1 llffylampf 10

RESULT 4

ID Y06007 standard; Peptide; 10 AA.

XX AC Y06010;

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.

XX KW Homo sapiens.

XX PN WO9918206-A2.

XX PD 15-APR-1999.

XX PR 21-SEP-1998; 98WO-US19609.

XX PR 08-OCT-1997; 97US-0061428.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PT 1999-277270/23.

XX PI Rosenberg SA, Wang RF;

XX DR 1999-277270/23.

XX PS Cancer antigen NY ESO1/CAG-3

XX Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y05988-Y06017) were identified. The present peptide (ranked 20) corresponds to amino acid residues 93-102 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

SQ Sequence 10 AA;

CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX Sequence 10 AA;

Query Match 57.1%; Score 52; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 9 AMPFATPMEA 18
|||||||
Db 1 ampfatpmea 10

RESULT 5

ID Y06010 standard; Peptide; 10 AA.

XX XX

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX XX

XX DE Human cancer antigen NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA.

XX KW Homo sapiens.

XX PN WO9918206-A2.

XX PD 15-APR-1999.

XX PR 21-SEP-1998; 98WO-US19609.

XX PR 08-OCT-1997; 97US-0061428.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PT 1999-277270/23.

XX PI Rosenberg SA, Wang RF;

XX DR 1999-277270/23.

XX PS Cancer antigen NY ESO1/CAG-3

XX Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see X58599). 30 Epitopes (see Y05988-Y06017) were identified. The present peptide (ranked 20) corresponds to amino acid residues 93-102 of CAG-1 ORF1 (see Y05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see Y05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX Sequence 10 AA;

RESULT 8
 DE Human MAP kinase SAPK3 peptide fragment.
 B12647 XX
 ID B12647 standard; peptide; 11 AA.
 XX
 AC B12647;
 XX DT 13 - NOV - 2000 (first entry)
 XX Protein kinase peptide ERK6 human.
 XX
 KW Protein kinase; P38-gamma; crystallised P38 complex; structure;
 protein co-ordinate data; inhibitor; identification.
 XX OS Homo sapiens.
 XX WO200036096-A1.
 PN 18 - NOV - 1999.
 XX PF 04 - MAY - 1999; 99WO-GB01385.
 XX PR 09 - MAY - 1998; 98GB-0009869.
 XX PA (MEDI -) MEDICAL RES COUNCIL.
 PI Cohen P, Goedert M, Eyers PA;
 XX DR WPI: 2000 - 038954/03.
 XX PT Inhibiting particular protein kinases that have non-bulky residue in
 the ATP binding site using pyridinyl-imidazole derivative, e.g. for
 reducing deposition of extracellular matrix -
 XX PS Example 1; Fig 1; 91pp; English.
 XX CC The invention relates to inhibiting a protein kinase (I) that has Thr (or
 a residue less bulky than Thr) at the position equivalent to Thr 106 in
 SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.
 CC The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used
 therapeutically: (i) to treat extracellular matrix (ECM) deposition, to
 encourage tissue regeneration and/or repair, tissue remodelling and
 healing of wounds or injuries, also to reduce scar tissue formation
 following a brain injury; (ii) to treat patients with (or at risk of
 developing) end-stage organ failure, pathological ECM accumulation,
 (renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney
 damage; (iii) to treat defects of bone growth or homeostasis (e.g.
 osteoporosis), arthritis and atherosclerosis in which transforming growth
 factor beta (but not proinflammatory cytokines) are implicated, and (iv)
 to treat epithelial, mesenchymal or glial cancers, solid tumors,
 melanomas, small cell lung cancer, chronic myelogenous leukemia,
 (including purging bone marrow of affected cells) and T cell lymphoma.
 CC Transgenic animals (or transfected cells) that include a protein kinase
 located at the position equivalent to 106 are used to determine
 the physiological role of the kinase and to identify its substrates, and
 the protein kinase can be used to screen for drugs (or lead compounds).
 CC The inhibitors are specific for the (I), i.e. they do not inhibit similar
 protein kinases in which the position equivalent to Thr 106 is occupied
 by Met or some other bulky residue.
 XX SQ Sequence 15 AA;
 XX

Query Match Score 37; DB 21; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.4;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 EFYLAMPF 12
 :||| |||
 2 dfylvmpf 9

RESULT 9
 Y66484 Query Match Score 40.7%; DB 21; Length 15;
 ID Y66484 standard; peptide; 15 AA.
 XX AC Y66485;
 XX DT 07 - MAR - 2000 (first entry)

Query Match Score 37; DB 21; Length 15;
 Best Local Similarity 75.0%; Pred. No. 4.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 EFYLAMPF 12
 :||| |||
 3 dfylvmpf 10

RESULT 10
 Y66485 Query Match Score 40.7%; DB 21; Length 15;
 ID Y66485 standard; peptide; 15 AA.
 XX AC Y66485;
 XX DT 07 - MAR - 2000 (first entry)

DE	Human MAP kinase SAPK4 peptide fragment.	DE	Human MAP kinase SAPK3 peptide fragment.
XX	Protein kinase; inhibitor; extracellular matrix deposition; ECM; cancer;	XX	Protein kinase; inhibitor; extracellular matrix deposition; ECM; cancer;
KW	tissue remodelling; wound healing; injury; fibrosis;	KW	tissue regeneration; tissue remodelling; wound healing; injury; fibrosis;
KW	immunosuppression; diabetic nephropathy; and kidney damage; bone growth;	KW	immunosuppression; diabetic nephropathy; and kidney damage; bone growth;
KW	MAP kinase; osteoporosis; arthritis; atherosclerosis; cytokine; tumor.	KW	MAP kinase; osteoporosis; arthritis; atherosclerosis; cytokine; tumor.
XX	OS Homo sapiens.	XX	OS Homo sapiens.
XX	PN WO958128-A1.	XX	PN WO958128-A1.
XX	PD 18-NOV-1999.	XX	PD 18-NOV-1999.
XX	PF 04-MAY-1999; 99WO-GB01385.	XX	PF 04-MAY-1999; 99WO-GB01385.
XX	PR 09-MAY-1998; 98GB-0009869.	XX	PR 09-MAY-1998; 98GB-0009869.
XX	(MEDI-) MEDICAL RES COUNCIL.	XX	(MEDI-) MEDICAL RES COUNCIL.
XX	PA Cohen P, Goedert M, Evers PA;	XX	PA Cohen P, Goedert M, Evers PA;
PI	DR WPI; 2000-038954/03.	PI	DR WPI; 2000-038954/03.
XX	PT Inhibiting particular protein kinases that have non-bulky residue in	XX	PT Inhibiting particular protein kinases that have non-bulky residue in
PT	the ATP binding site using pyridinyl-imidazole derivative, e.g. for	PT	the ATP binding site using pyridinyl-imidazole derivative, e.g. for
PT	reducing deposition of extracellular matrix	PT	reducing deposition of extracellular matrix
XX	PS Example 1; Fig 1; 93pp; English.	XX	PS Example 1; Fig 1; 93pp; English.
XX	CC The invention relates to inhibiting a protein kinase (I) that has Thr (or	CC	The invention relates to inhibiting a protein kinase (I) that has Thr (or
CC	a residue less bulky than Thr) at the position equivalent to Thr 106 in	CC	a residue less bulky than Thr) at the position equivalent to Thr 106 in
CC	SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.	CC	SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor.
CC	The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used	CC	The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used
CC	therapeutically: (i) to treat extracellular matrix (ECM) deposition, to	CC	therapeutically: (i) to treat extracellular matrix (ECM) deposition, to
CC	encourage tissue regeneration and/or repair, tissue remodelling and	CC	encourage tissue regeneration and/or repair, tissue remodelling and
CC	healing of wounds or injuries, also to reduce scar tissue formation	CC	healing of wounds or injuries, also to reduce scar tissue formation
CC	following a brain injury; (ii) to treat patients with (or at risk of	CC	following a brain injury; (ii) to treat patients with (or at risk of
CC	developing) end-stage organ failure, pathological ECM accumulation,	CC	developing) end-stage organ failure, pathological ECM accumulation,
CC	(renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney	CC	(renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney
CC	damage; (iii) to treat defects of bone growth or homeostasis (e.g.	CC	damage; (iii) to treat defects of bone growth or homeostasis (e.g.
CC	osteoporosis), arthritis and atherosclerosis in which transforming growth	CC	osteoporosis), arthritis and atherosclerosis in which transforming growth
CC	factorbeta (but not proinflammatory cytokines) are implicated, and (iv)	CC	factorbeta (but not proinflammatory cytokines) are implicated, and (iv)
CC	to treat epithelial, mesenchymal or glial cancers, solid tumors,	CC	to treat epithelial, mesenchymal or glial cancers, solid tumors,
CC	melanomas, small cell lung cancer, chronic myelogenous leukemia	CC	melanomas, small cell lung cancer, chronic myelogenous leukemia
CC	(including purging bone marrow of affected cells) and T cell lymphoma.	CC	(including purging bone marrow of affected cells) and T cell lymphoma.
CC	transgenic animals (or transfected cells) that include a protein kinase	CC	transgenic animals (or transfected cells) that include a protein kinase
CC	in which the position equivalent to 106 is mutated are used to determine	CC	in which the position equivalent to 106 is mutated are used to determine
CC	the physiological role of the kinase and to identify its substrates, and	CC	the physiological role of the kinase and to identify its substrates, and
CC	the protein kinase can be used to screen for drugs (or lead compounds).	CC	the protein kinase can be used to screen for drugs (or lead compounds).
CC	The inhibitors are specific for the (I), i.e. they do not inhibit similar	CC	The inhibitors are specific for the (I), i.e. they do not inhibit similar
CC	protein kinases in which the position equivalent to Thr 106 is occupied	CC	protein kinases in which the position equivalent to Thr 106 is occupied
XX	CC by Met or some other bulky residue.	CC	CC by Met or some other bulky residue.
XX	Sequence 15 AA;	XX	Sequence 15 AA;
SQ.	Query Match 40.7%; Score 37; DB 21; Length 15;	Query Match 40.7%; Score 37; DB 21; Length 15;	
	Best Local Similarity 75.0%; Pred. No. 4.7;	Best Local Similarity 75.0%; Pred. No. 4.7;	
	Matches 1; Mismatches 1; Indels 0; Gaps 0;	Matches 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	5 EFYLMAMPF 12 : 3 dfy1vmpf 10	Qy 5 EFYLMAMPF 12 : 3 dfy1vmpf 10	
Db	RESULT 11 Y66509 ID Y66509 standard; peptide; 15 AA. XX AC Y66509; XX DT 07-MAR-2000 (first entry)	RESULT 12 Y66510 ID Y66510 standard; peptide; 15 AA. XX AC Y66510; XX DT 07-MAR-2000 (first entry)	

Human MAP kinase SAPK4 peptide fragment.

XX Protein kinase; inhibitor; extracellular matrix deposition; ECM; cancer; tissue regeneration; tissue remodelling; wound healing; injury; fibrosis; immunosuppression; diabetic nephropathy; and kidney damage; bone growth; MAP kinase; osteoporosis; arthritis; atherosclerosis; atherosclerosis; tumor. OS Homo sapiens.

XX WO958128-A1.

XX PD 18-NOV-1999.

XX PF 04-MAY-1999; 99WO-GB01385.

PR 09-MAY-1998; 98GB-0009869.

XX (MEDI-) MEDICAL RES COUNCIL.

PA Cohen P, Goedert M, Eyers PA;

PI Chen Y, Gure A,

XX DR 2000-038954/0.

XX PT Inhibiting particular protein kinases that have non-bulky residue in the ATP binding site using Pyridinyl-imidazole derivative, e.g. for reducing deposition of extracellular matrix -

XX PS Example 1; Fig 1; 93pp; English.

XX The invention relates to inhibiting a protein kinase (I) that has Thr (or a residue less bulky than Thr) at the position equivalent to Thr 106 in SAPK2a/p38 by treatment with a pyridinyl-imidazole, or related inhibitor. The (I) is not SAPK2a/p38 or SAPK2b/p38beta2. The inhibitors are used therapeutically: (i) to treat extracellular matrix (ECM) deposition, to encourage tissue regeneration and/or repair, tissue remodelling and healing of wounds or injuries, also to reduce scar tissue formation following a brain injury; (ii) to treat patients with (or at risk of developing) end-stage organ failure, pathological ECM accumulation, (renal) fibrosis, immunosuppression, diabetic nephropathy, and kidney damage; (iii) to treat defects of bone growth or homeostasis (e.g. osteoporosis), arthritis and atherosclerosis in which transforming growth factorbeta (but not proinflammatory cytokines) are implicated, and (iv) to treat epithelial, mesenchymal or giant cancer, solid tumors, melanomas, small cell lung cancer, chronic myelogenous leukemia, (including purging bone marrow of affected cells) and T cell lymphoma. Transgenic animals (or transfected cells) that include a protein kinase in which the position equivalent to 106 is mutated are used to determine the physiological role of the kinase and to identify its substrates, and the protein kinase can be used to screen for drugs (or lead compounds). The inhibitors are specific for the (I), i.e. they do not inhibit similar protein kinases in which the position equivalent to Thr 106 is occupied by Met or some other bulky residue.

XX Sequence 15 AA;

YQ 5 EFYLAMPF 12
:||| |||
Db 3 dflylmpf 10

Query Match Score 40.7%; DB 21; Length 15;
Best Local Similarity 75.0%; Pred. No. 4.7;
Matches 6; Conservative 1; Indels 0; Gaps 0;

DE NY-ESO-1 derived peptide #13.

XX Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1; HLA binding; human leukocyte antigen; cytolytic T cell; CTL; cytotoxic; melanoma; synovial sarcoma.

XX OS Homo sapiens.

XX PN WO200000824-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14493.

XX PR 26-JUN-1998; 98US-0105839.

XX (LUDW-) LUDWIG INST CANCER RES.

XX PA Turcic O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;

XX PI Chen Y, Gure A, Old LJ;

XX DR 2000-170933/15.

XX PT Determining the possible presence of breast, endometrial, colorectal, lung, bladder or head-neck cancer -

XX PS Example 13; Page 26; 40pp; English.

XX A method has been developed for determining the possible presence of a cancer, which is not melanoma or synovial sarcoma. The method comprises assaying a sample taken from the subject to determine the expression of an SSX gene, and determining the expression as a determination of the possible presence of cancer. Expression of SSX1 gene indicates possible presence of breast, endometrial, colorectal, lung, bladder or head-neck cancer. These cancers are also detected by SSX2 and SSX4 gene expression. SSX2 gene expression additionally indicates possible presence of lymphoma, renal cell cancer, glioma and prostate cancer. Expression of SSX4 gene also indicates possible presence of ovarian or stomach cancer. SSX5 gene expression indicates the same cancers as SSX1, except breast cancer. Determining expression of SSX gene can be used to monitor progress of melanoma or synovial sarcoma which is not cancer. The SSX-derived peptide complex stimulates proliferation of cytolytic T cells. This is useful for treating cancer, especially melanoma. Y78464 to Y79468 represent specifically claimed HIA binding peptides for use in the method of the invention. Z88452 to Z88465 represent PCR primers used in the isolation of SSX genes in the exemplification of the present invention. Y78469 to Y78500, and Y79384 to Y79762 represent peptides derived from SSX proteins or NY-ESO-1, which are used in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match Score 36; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FATPMEA 18
| | | | | |
Db 1 fatpmea 7

RESULT 14

R49308 ID R49308 standard; Protein: 17 AA.
XX AC R49308;
XX DT 16-SEP-1994 (first entry)
XX DE Transferrin receptor position 680-696.
XX KW Naturally-occurring; immunomodulatory protein; human; therapy; class I;

RESULT 13
Y79757 ID Y79757 standard; Peptide; 9 AA.
XX AC Y79757;
XX DT 10-MAY-2000 (first entry)

KW major histocompatibility complex; class II; allotype; type I diabetes;
 KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
 KW multiple sclerosis; transplant rejection; vaccine; MHC.
 XX Homo sapiens.
 XX W09404171-A.
 XX 03-MAR-1994.
 XX PF 11-AUG-1993; 93WO-US07545.
 XX PR 11-AUG-1992; 92US-0925460.
 PR 15-JUN-1993; 93US-0925460.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Chicz RM, Hedley ML, Stern LJ, Strominger JL, Urban RG;
 Vignal DA;
 XX DR 1994-082825/10.
 XX Novel immunomodulatory peptide(s) and nucleic acids - useful for
 treatment of auto:immune diseases, transplant rejection and for
 vaccination
 XX Disclosure: Page 36; 139pp; English.
 CC The sequences given in R46981-7038 represent peptide
 fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human
 major histocompatibility complex (MHC) class II allotype. These
 CC peptides may be used for therapy of autoimmune diseases, such as
 type I diabetes, rheumatoid arthritis and multiple sclerosis, and to
 reduce transplant rejection. They may also be used for vaccination
 providing an exclusively T cell-mediated response, which can be
 class I or class-II based, or both, depending on the length and
 character of the immunogenic peptides.
 XX Sequence 17 AA;
 SQ

Query Match 35.2%; Score 32; DB 15; Length 17;
 Best Local Similarity 26.7%; Pred. No. 39;
 Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 4 LEFFYLAMPATPMEA 18
 :|:|:|:|:
 Db 2 veyfflspvyspk 16

RESULT 15
 WI0317
 ID WI0317 standard; peptide: 16 AA.
 XX AC WI0317;
 XX DT 13-MAR-1997 (first entry)

DE Beta-subtype retinoic acid receptor, residues 11-26.
 XX KW Beta-subtype; retinoic acid; receptor; beta-RAR;
 KW amino-terminus; antibody; detection; immunoprecipitation assay;
 KW epitope; tumour.
 XX Homo sapiens.

XX FH Key Location/Qualifiers
 FT Misc_difference 16
 FT /note= "Cys added to natural sequence for KLH
 conjugation"
 XX US5585244-A.

XX PD 17-DEC-1996.
 XX PF 10-JUN-1994; 94US-0258851.
 XX PR 10-JUN-1994; 94US-0258851.
 XX PA (LIGA-) LIGAND PHARM INC.
 XX PI Allegretto EA, Pike JW;
 XX DR WPI: 1997-051173/05.
 XX PT Antibody to gamma sub-type retinoid X receptor - useful for
 detecting receptor, esp. in tumour samples
 XX PS Example 1; Columns 9-10; 20pp; English.
 XX CC The present peptide comprises residues 11-26 of the beta-subtype
 CC retinoic acid receptor (beta-RAR), N-terminus. It can be
 used to generate antibodies for the detection of beta-RAR, which
 CC following an immunoprecipitation assay was found to be present in
 CC HL60 (human promyelocytic carcinoma) cell, HeLa S3 (human cervical
 CC carcinoma) cell, Hep G2 (human hepatoma) cell, MCF-7 (human breast
 CC carcinoma) cell minus beta-E2, MCF-7 cell plus beta-E2, MCF-7
 CC tumor plus beta-E2 and ME-180 (human cervical carcinoma) tumour
 CC extracts at respective levels of not determined, 9, 5, not
 CC determined, not determined, not determined and not determined
 CC fmol/ml.
 XX SQ Sequence 16 AA;
 CC Query Match 34.1%; Score 31; DB 18; Length 16;
 CC Best Local Similarity 50.0%; Pred. No. 54;
 CC Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RLLEFFYLAMP 11
 DB 4 qildiytasp 13

Search completed: May 8, 2001, 15:07:10
 Job time: 226 sec

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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:08:21 ; Search time 68.24 Seconds
(without alignments)
18.127 Million cell updates/sec

Title: US-09-165-546A-12

Perfect score: 91

Sequence: 1 SRLLEFYLAMPFAFPMEA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 4929

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_67;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	29.7	15	B45115	Peptidylprolyl iso
2	26	28.6	13	PH1596	Ig H chain V-D-J r
3	25	27.5	24	T08160	S locus-linked pro
4	24	26.4	25	B36934	orf3' of mada -
5	23	25.3	13	PH1593	Ig H chain V-D-J r
6	23	25.3	15	B61457	alpha-glucosidase
7	23	25.3	18	A48550	hexon - canine ade
8	23	25.3	18	B49048	T-cell receptor be
9	23	25.3	20	S78760	ribosomal protein
10	23	25.3	20	PX0061	beta-N-acetylgluco
11	23	25.3	25	S78343	hypothetical prote
12	23	25.3	25	S39360	CDK inhibitor - mo
13	22	24.2	19	S32675	nitrogen fixation
14	22	24.2	23	A53631	H+ - transporting AT
15	22	24.2	24	S69081	GDNF receptor alph
16	22	24.2	24	S38766	petroglaucin - pet
17	22	24.2	25	S21204	H+ - transporting AT
18	22	24.2	25	S69139	bumentanide-binding
19	21	23.1	14	S09721	2S albumin small C
20	21	23.1	14	PA0104	protein QF200070 -
21	21	23.1	14	C48394	major fat-globule
22	21	23.1	15	LFECF	phe operon leader
23	21	23.1	16	PH1580	Ig H chain V-D-J r
24	21	23.1	16	S68730	bleomycin-binding
25	21	23.1	18	PH1368	Ig heavy chain DJ
26	21	23.1	18	A59137	protein Pil - gold
27	21	23.1	20	C56894	intracrystalline C
28	21	23.1	20	B56894	intracrystalline C
29	21	23.1	21	PH1730	Ig heavy chain V r

ALIGNMENTS

RESULT 1

B45115 Peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)

N;Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase F

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997

C;Accession: B45115

R;Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calhycay, J.; Boulton J. Biol. Chem. 267, 21753-21760, 1992

A;Title: Characterization of high molecular weight FK-506 binding activities reveals

A;Reference number: A45115; MUID:93016131

A;Accession: B45115

A;Status: Preliminary

A;Molecule type: protein

A;Residues: 1-15 <WIE>

A;Experimental source: JURKAT cells

A;Note: sequence extracted from NCBI backbone (NCBIP:116748)

C;Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 29.7%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy YLAMPFA 13
Db YLAPPYA 13

RESULT 2

PH1596 Ig H chain V-D-J region (wild-type clone 303) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1596

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less m

A;Reference number: PH1580; MUID:93301609

A;Accession: PH1596

A;Molecule type: DNA

A;Residues: 1-13 <LEV>

C;Keywords: immunoglobulin

Query Match 28.6%; Score 26; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2e-02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy SRLLEFYLAMPF 12
Db :| :|| :

Db 2 ARRLGGYYAMDY 13

RESULT 3

T08160 S locus-linked protein SLL1b - rape
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000
C;Accession: T08160
R;Yu, K.; Schauer, U.; Glavin, T.L.; Goring, D.R.; Rothstein, S.J.
Plant Cell 8: 2369-2380, 1996
A;Title: Molecular characterization of the S locus in two self-incompatible *Brassica* napus
A;Reference number: 216388; MUID:97143881
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-24 <TUK>
A;Cross-references: EMBL:U66192; NID:91518109; PIDN:AAB49422.1; PID:91518111

Query Match Score 23; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 6.7e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 1 SRLEFFYLAMPF 12

RESULT 6

B61457 alpha-D-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
C;Species: Tetrahymena pyriformis
C;Accession: B61457
C;Date: 28-Oct-1994 #sequence_revision 28-oct-1994 #text_change 07-Dec-1999
R;Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A;Title: A thermostable acid alpha-D-glucosidase from *Tetrahymena thermophila*: purification
A;Reference number: A61457; MUID:90095388
A;Accession: B61457
A;Molecule type: protein
A;Residues: 1-15 <BAN>
C;Genetics:
A;Genetic code: ScC5
C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; mo-

Query Match Score 23; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 7.8e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 5 EFYIAMP 11

RESULT 4

B36934 orf3' of mada - *Thiobacillus versutus*. (fragment)
C;Species: *Thiobacillus versutus*
C;Accession: B36934
R;Huittema, F.; van Beurmen, J.; van Driessche, G.; Duine, J.A.; Canters, G.W.
J. Bacteriol. 175, 6254-6259, 1993
A;Title: Cloning and sequencing of the gene coding for the large subunit of methylamine
A;Reference number: A36934; MUID:94012487
A;Accession: B36934
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 <HGT>
A;Experimental source: ATCC 25364T
A;Note: sequence extracted from NCBI backbone (NCBIN:138060, NCBIPI:138062)

Query Match Score 23; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 9 QFYIAMPV 15

Query Match Score 23; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 7.8e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 11 PFATPME 17

RESULT 7

A48550 canine adenovirus 1 (fragment)
hexon - canine adenovirus cani (canine adenovirus 1)
C;Species: Mastadenovirus cani (canine adenovirus 1)
C;Accession: A48550
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 26-Aug-1999
R;Cairi, F.; Weber, J.M.
Virus Genes 6, 307-312, 1992
A;Title: Nucleotide and deduced amino acid sequence of the canine adenovirus type 1 p
A;Reference number: A48550; MUID:93033182
A;Accession: A48550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <CAI>
A;Cross-references: GB:M72715; PIDN:AAA42528.1; PID:g210023
A;Note: sequence extracted from NCBI backbone (NCBIN:114644; NCBIPI:114646)
C;Superfamily: adenovirus hexon protein

Query Match Score 23; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 4 LEFYIAMPFAT 14

RESULT 8

B49048 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Accession: B49048
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
R;Sjöstrand, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juven-

Db 14 LRSFLAAALFAT 24

Query Match Score 23; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 5 PH1593

RESULT 9

Ig H chain V-D-J region (wild-type clone 144) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: PH1593
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-les mice
A;Reference number: PH1580; MUID:93301609
A;Molecule type: DNA
A;Residues: 1-13 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

A;Reference number: A49048; MUID:92387250
 A;Accession: B49048
 A;Status: Preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-18 <SIO>
 A;Experimental source: Patient EV, IL-2R+ synovial T-cells
 A;Note: sequence extracted from NCBI backbone (NCBIP:113264)
 C;Keywords: T cell receptor

Query Match 9
 Best Local Similarity 25.3%; Score 23; DB 2; Length 18;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 FYLAMP 11
 Db 4 FYLCAP 9

RESULT 9
 S78760 ribosomal protein MRP-14, mitochondrial - bovine (fragments)
 C;Species: Bos primigenius taurinus (cattle)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C;Accession: S78760
 R;Graack, H.R.
 submitted to the Protein Sequence Database, July 1999
 A;Reference number: S78760
 A;Accession: S78760
 A;Molecule type: protein
 A;Residues: 1-11;12-20 <GRAs>
 C;Keywords: mitochondrial

Query Match 9
 Best Local Similarity 25.3%; Score 23; DB 2; Length 20;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 RLDEFY 7
 Db 11 RLAEYY 16

RESULT 10
 PX0061 beta-N-acetylglucosaminylglycopeptide beta1,4-galactosyltransferase (EC 2.4.1.38) - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 03-Mar-1995
 C;Accession: PX0061
 R;Kawano, J.; Oinuma, T.; Nakayama, T.; Suganuma, T.
 J. Biochem. 111, 568-572, 1992
 A;Reference number: PX0061; MUID:92348341
 A;Accession: PX0061
 A;Molecule type: protein
 A;Residues: 1-20 <KAW>
 A;Experimental source: liver microsome
 C;Comment: This enzyme catalyzes the transfer of galactose from an activated UDP-galactose to lactose synthase (EC 2.4.1.38). The complex of this enzyme and alpha-lactalbumin is lactose synthase hexosyltransferase;
 C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 10
 Best Local Similarity 25.3%; Score 23; DB 2; Length 20;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 9 AMPFATPNEA 18
 Db 1 AMGATQRA 10

RESULT 11
 S73343 hypothetical protein 25 - Odontella sinensis chloroplast
 C;Species: chloroplast Odontella sinensis
 C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 24-Apr-1998
 C;Accession: S73343
 R;Kowallik, K.V.; Stoebbe, B.; Schaffran, I.; Kroth-Pancic, P.; Freiber, U.
 Plant Mol. Biol. Rep. 13, 336-342, 1995
 A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sine
 A;Reference number: S78238
 A;Accession: S78238
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-25 <KOW>
 A;Cross-references: EMBL:Z67753; NID:91185127; PID:e211881; PID:91185233
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
 C;Genetics:
 A;Genome: chloroplast
 C;Keywords: chloroplast

Query Match 9
 Best Local Similarity 25.3%; Score 23; DB 2; Length 25;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 LEFYLLAM 10
 Db 4 ISFYIAL 10

RESULT 12
 S39360 CDK inhibitor - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: S39360
 R;Gu, Y.; Turck, C.W.; Morgan, D.O.
 Nature 366, 707-710, 1993
 A;Title: Inhibition of CDK2 activity *in vivo* by an associated 20K regulatory subunit.
 A;Reference number: S39360; MUID:94081957
 A;Accession: S39360
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-25 <GYV>

Query Match 9
 Best Local Similarity 25.3%; Score 23; DB 2; Length 25;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 LLEFYLLAMPFATP 15
 Db 4 LTDFFHSSKVILSP 16

RESULT 13
 S32675 nitrogen fixation protein nifB - *Anabaena variabilis* (fragment)
 C;Species: Anabaena variabilis
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
 C;Accession: S32675
 R;Monnerjahn, U.; Boehme, H.
 submitted to the EMBL Data Library, December 1992
 A;Description: Cloning and expression in *E. coli* of the *Anabaena*.
 A;Accession number: S32675
 A;Accession: S32675
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-19 <MON>
 A;Cross-references: EMBL:X69898; NID:9296503; PIDN:CAA49521.1; PID:9296504
 C;Genetics:
 A;Gene: nifB
 C;Superfamily: Rhizobium nifB protein

RESULT 14
 S73343

Query Match 24.2%; Score 22; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 LEFY 7
 | | |
 Db 10 LEFY 13

RESULT 14
 A53631
 H+-transporting ATP synthase (EC 3.6.1.34) beta chain - thermophilic bacterium PS-3 (Fré
 C; Species: thermophilic bacterium PS-3
 C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 17-Mar-1999
 C; Accession: A53631
 R; Paik, S.-K.; Jault, J.M.; Allison, W.S.
 Biochemistry 33, 126-133, 1994
 A; Title: Inhibition and inactivation of the F-1 adenosinetriphosphatase from Bacillus. PS
 A; Reference number: A53631; MUID:94114474
 A; Accession: A53631
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-23 <PAl>
 C; Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al
 C; Keywords: ATP biosynthesis; hydrolase

Query Match 24.2%; Score 22; DB 2; Length 23;
 Best Local Similarity 33.3%; Pred. No. 1.8e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 LEFYLAMPF 12
 | : | : |
 Db 2 IQLFLSONF 10

RESULT 15
 S69080
 GDNF receptor alpha chain, precursor - rat (fragment)
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 12-Feb-1998 #sequence_revision 31-Jan-2000 #text_change 31-Jan-2000
 C; Accession: S69080
 R; Treanor, J.J.S.; Goodman, L.; de Sauvage, F.; Stone, D.M.; Poulsen, K.T.; Beck, C.D.;
 vies, A.M.; Asai, N.; Takahashi, M.; Vandlen, R.; Henderson, C.E.; Rosenthal, A.
 Nature 382, 80-83, 1996
 A; Title: Characterization of a multicomponent receptor for GDNF.
 A; Reference number: S69080; MUID:96273032
 A; Accession: S69080
 A; Molecule type: mRNA
 A; Residues: 1-24 <TRE>
 F; 1-24/Domain: signal sequence #status predicted <SIG>

Query Match 24.2%; Score 22; DB 2; Length 24;
 Best Local Similarity 44.4%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 LLFEYIAMP 11
 | : | : |
 Db 3 LATLIFALP 11

Search completed: May 8, 2001, 15:08:22
 Job time: 293 sec

Title:	US-09-165-546A-12	Score:	34	18	19.8	22	1	VGLG_RABVA
Sequence:	1 SRILEFFYLAMPFATPMEA 18		35	18	19.8	24	1	DNAJ_STRAG
Scoring table:	BLOSUM62		36	18	19.8	24	1	HEMULINRE
Searched:	Gapop 10.0 , Gapext. 0.5		37	18	19.8	24	1	PQQA_PSEFL
Total number of hits satisfying chosen parameters:	1423		38	18	19.8	25	1	NP4_HUMAN
Minimum DB seq length: 0			39	17	18.7	8	1	ALL_CARMA
Maximum DB seq length: 25			40	17	18.7	10	1	ANGI_BOTJA
Post-processing: Minimum Match 0%			41	17	18.7	10	1	LPK2_LOCMI
Maximum Match 100%			42	17	18.7	11	1	LPW_THETH
Listing first 45 summaries			43	17	18.7	13	1	YPNP_PHOL
Database :	SwissProt_39:*		44	17	18.7	14	1	HY14_PIG
			45	17	18.7	15	1	ACEA_ACICA
ALIGNMENTS								
Scoring table:	BLOSUM62		RESULT 1					
Searched:	Gapop 10.0 , Gapext. 0.5		ID ECDC_LYMDI					
Total number of hits satisfying chosen parameters:	1423		AC P80940;					
Minimum DB seq length: 0			DT 15-JUL-1998 (Rel. 36, Created)					
Maximum DB seq length: 25			DT 15-JUL-1998 (Rel. 36, Last sequence update)					
Post-processing: Minimum Match 0%			DT 15-JUL-1998 (Rel. 36, Last annotation update)					
Maximum Match 100%			DE TESTIS ECDSIOTROPIN PEPTIDE C (TE).					
Listing first 45 summaries			OS Lymantria dispar (Gypsy moth).					
Database :	SwissProt_39:*		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
			OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;					
			OC Noctuoidea; Lymantriidae; Lymantria;					
			OX NCBI_TaxID=13123;					
			RN [1]					
			RP SEQUENCE.					
			RC TISSUE;Brain;					
			RX MEDLINE=97387807; Published=9243792;					
			RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,					
			RA Bell R.A.;					
			RT "Naturally occurring analogs of Lymantria testis ecdisiotropin, a gonadotropin isolated from brains of Lymantria dispar pupae."					
			RT gonadotropin isolated from brains of Lymantria dispar pupae."					
			RL Arch. Insect Biochem. Physiol. 36:37-50(1997).					
			CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDSIOTROPIN IN THE TESTES					
			CC OF LARVAE AND PUPAE.					
			SQ SEQUENCE 14 AA; 1553 MW; 17E479531A6856BB CRC64;					
			Query Match 26.4%; Score 24; DB 1; Length 14;					
			Best Local Similarity 57.1%; Pred. No. 3 5e+02;					
			Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
			QY 7 YLAMPFA 13					
			Db 7 YTPLPFA 13					
Result No.	Score	Query Match	Length	DB ID	Description			
1	24	26.4	14	1 ECDC_LYMDI	P80940 lymantria d			
2	23	25.3	18	1 HEX_ABECU	P35985 canine aden			
3	23	25.3	25	1 YCX8_QODOSI	P49334 odontella s			
4	22	24.2	14	1 MARL_ALTSP	P29399 alteromonas			
5	22	24.2	19	1 ADC_CLOPA	P81336 clostridium			
6	22	24.2	25	1 ATP0_SPIOL	P80982 spinacia ol			
7	21	23.1	15	1 LPE_ECOLI	P03057 escherichia			
8	21	23.1	15	1 UNO1_DINPS	P81106 pinus pinas			
9	21	23.1	22	1 ATP6_COTUJA	P50811 coturnix co			
10	21	23.1	25	1 BGBP_PENVA	P81182 penaeus van			
11	20	22.0	13	1 CRBL_CASP	P17327 icaria sp.			
12	20	22.0	18	1 DRPH_UCAPU	P08811 uca pugilat			
13	20	22.0	20	1 SODE_PASPI	P81527 pastuerella			
14	20	22.0	25	1 SMBP_RAT	P80968 rattus norv			
15	19	20.9	25	1 YIGI_SALTY	P40725 salmonella			
16	19	20.9	9	1 MGMT_BOVIN	P29177 bos taurus			
17	19	20.9	10	1 COXO_SHEEP	P80337 ovis aries			
18	19	20.9	12	1 PA2B_VIPBO	P31059 viper beru			
19	19	20.9	13	1 LMT4_LOCMI	P41190 locusta mig			
20	19	20.9	15	1 MCRA_METTE	P22448 methanosa			
21	19	20.9	16	1 ANPB_ELEGIR	P11221 eleginus gr			
22	19	20.9	19	1 DHAB_COMTE	P80704 comamonas t			
23	19	20.9	20	1 DPP4_BOVIN	P81225 bos taurus			
24	19	20.9	21	1 YD90_HAEIN	P45194 haemophilus			
25	19	20.9	25	1 ANT3_MESAU	P81050 mesocetoceti			
26	18	19.8	8	1 UPAA_HUMAN	P30966 homo sapien			
27	18	19.8	10	1 NS1_MYCTU	P81135 mycobacteri			
28	18	19.8	11	1 PQQC_PSEFL	P55173 pseudomonas			
29	18	19.8	17	1 ATP1_PAVLO	P28529 pavlova lut			
30	18	19.8	19	1 ANP7_ELEGIR	P11320 eleginus gr			
31	18	19.8	21	1 ODP2_SOILTU	P81221 solanum tub			
32	18	19.8	22	1 LANM_STRMU	P80666 streptococc			
33	18	19.8	22	1 ODPX_BOVIN	P22439 bos taurus			

-1- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE

Mastadenovirus.

NCBI_TaxID=36364;

SEQUENCE FROM N. A. Cai F., Weber J. M.;

Medline=93033182; PubMed=1413543;

"Nucleotide and deduced amino acid sequence of the canine adenovirus type 1 proteinase";

Virus Genes 6:307-312(1992).

-1- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE

CC VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
 CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).

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DR EMBL; M72715; AAA42528.1; -;
 DR PIR; A48550; A48550.
 DR HSSP; P03277; 1DIXX.
 KW Coat protein; Hexon protein; Late protein.
 FT NON_TER 1 1 MW; B9E2AE307A420962 CRC64;
 SQ SEQUENCE 18 AA; 1938 MW;

Query Match	25.3%	Score 23;	DB 1;	Length 18;
Best Local Similarity	57.1%	Pred. No.	6.6e+02;	
Matches	4;	Mismatches	2;	Indels 0;
				Gaps 0;

QY 7 YLAMPFA 13
 Db 6 YLRTPEFS 12

RESULT 3
 YCX8_ODOSI STANDARD PRT; 25 AA.
 ID YCX8_ODOSI STANDARD PRT; 25 AA.
 AC P49834; 34, Created
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHETICAL 3.1 KDa PROTEIN IN PSBJ-TRNE INTERGENIC REGION (ORF25).
 OG Chloroplast.
 OC Eukaryota; stramenopiles; Bacillariophyta; Coccinodiscophyceae;
 OC Biddulphiophyceae; Eupodiscaceae; Odontella; Odontella sinensis.
 OX NCBI_TAXID=2839;

RN [1]
 RA Kowallik K.V.; Stoabe B.; Schaffran I.; Kroth-Pancic P.; Freier U.;
 RT "the chloroplast genome of a chlorophyll a+c-containing alga,
 Odontella sinensis";
 RT Plant Mol. Biol. Rep. 13:336-342(1995).
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DR Z67753; CAA91776.1; -;
 KW Chloroplast; Hypothetical protein.
 SQ SEQUENCE 25 AA; 3083 MW;

Query Match	25.3%	Score 23;	DB 1;	Length 25;
Best Local Similarity	42.9%	Pred. No.	9.1e+02;	
Matches	3;	Mismatches	1;	Indels 0;
				Gaps 0;

QY 4 LEFYIYLAM 10
 Db 4 ISFYIYL 10

Query Match	25.3%	Score 23;	DB 1;	Length 25;
Best Local Similarity	42.9%	Pred. No.	9.1e+02;	
Matches	3;	Mismatches	1;	Indels 0;
				Gaps 0;

QY 8 LAMMFATP 15
 Db 10 ISMPLTAP 17

AC P29399;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE MARINOSTATINS C-2, C-1 AND D
 OS Alteromonas sp. (strain B-10-31).
 OC Bacteria; Protoprobacteria; gamma subdivision; Alteromonadaceae;
 OC Alteromonas.
 OX NCBI_TAXID=29156;
 RN [1]
 RP SEQUENCE, AND ACTIVE SITE.
 RX MEDLINE=92176155; PubMed=1794974;
 RA Takeno R.; Imada C.; Kamei K.; Hara S.;
 RT "The reactive site of marinostatin, a proteinase inhibitor from
 marine Alteromonas sp. B-10-31.";
 RT J. Biochem. 110:856-858(1991).
 RL CC -1- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
 NOT TRYPSIN.
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF MARINOSTATIN C-2.
 KW Serine protease inhibitor.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 6 7 REACTIVE BOND.
 FT VARIANT 1 1 MISSING (IN MARINOSTATIN C-1).
 FT VARIANT 1 1 MISSING (IN MARINOSTATIN D).
 SQ SEQUENCE 14 AA; 1644 MW; 6E7CFF92E932E44 CRC64;

Query Match 24.2% Score 22; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFAT 14
 Db 2 PFAT 5

Query Match 24.2% Score 22; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PFAT 14
 Db 2 PFAT 5

RESULT 5
 ADC_CLOPA STANDARD PRT;
 ID ADC_CLOPA STANDARD PRT;
 AC P81336; 36, Created
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ACEOACETATE DECARBOXYLASE (EC 4.1.1.4) (ADC) (CP 28/CP 29)
 DE (FRAGMENT).
 GN ADC
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TAXID=1501;
 RN [1]
 RP SEQUENCE W5;
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=96299198;
 RA Flengsrød R.; Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequencing analysis of proteins from Clostridium pasteurianum W5.";
 RT Electrophoresis 19:802-806(1998).
 CC -1- CATALYTIC ACTIVITY: ACETOACETATE + H(+) = ACETONE + CO(2).
 CC -1- SUBUNIT: HOMODODECAMER (BY SIMILARITY).
 KW Lyase; Decarboxylase.
 FT NON-TER 19 19
 SQ SEQUENCE 19 AA; 2078 MW; 6ACDAA91103AEC31 CRC64;

Query Match 24.2% Score 22; DB 1; Length 19;
 Best Local Similarity 37.5%; Pred. No. 1e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 LAMMFATP 15
 Db 10 ISMPLTAP 17

[2]	RN	SEQUENCE FROM N.A.
	RP	RP
	RX	RX
	RA	MEDLINE=91072346; PubMed=22254312;
	RA	Gavin N., Davison B.E.;
	RT	"pheAO mutants of <i>Escherichia coli</i> have a defective pheA attenuator.";
	RL	J. Biol. Chem. 265:21532-21535(1990).
	RN	[3]
	SEQUENCE FROM N.A.	
	RP	
	RC	STRAIN=NK12 / MG1655;
	RX	MEDLINE=9712661; PubMed=9278503;
	RA	Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
	RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
	RA	Gregor J.J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
	RA	Mau B., Shao Y.
	RT	"The complete genome sequence of <i>Escherichia coli</i> K-12.";
	RL	Science 277:1453-1474(1997).
	C1	-1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
	CN	OF PHENYLALANINE.
	CC	
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	CC	
	DR	EMBL; V00314; CAA23600.1; -;
	DR	EMBL; M10431; AAA24329.1; -;
	DR	EMBL; M58024; AAQ62183.1; -;
	DR	EMBL; AE000346; AAC75647.1; -.
	DR	PIR; A03593; LPFCF.
	DR	PIR; B36494; B36494.
	DR	EcoGene; EG11271; phel.
	KW	Leader peptide.
	SQ	SEQUENCE 15 AA: 1924 MW: CFE14AE3BFF935EO CRC64;
	Query Match	Score 21; DB 1; Length 15;
	Best Local Similarity	33.3%; Pred. No. 1.2e+03;
	Matches 4;	Mismatches 6; Indels 0; Gaps 0;
	QY	4 LEFYLAMPFATPP 15
	DB	: :
		4 IPFFFAFFFTPP 15
	RESULT	8
	ID	UN01_PINPS
	AC	P81106;
	DT	15-JUL-1998 (Rel. 36, Created)
	DT	15-JUL-1999 (Rel. 36, Last sequence update)
	DT	15-JUL-1999 (Rel. 38, Last annotation update)
	DE	UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (S1247/S1248) (N150/N151)
	DE	(FRAGMENT).
	OS	Pinus pinaster (Maritime pine).
	CC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
	CO	Coniferopsida; Coniferales; Pinaceae; Pinus.
	CX	NCBI_TAXID=71647;
	RN	[1]
	SEQUENCE	
	RC	TISSUE=Needle;
	RA	Plomion C., Costa P., Bahrmann N., Frigerio J.M.;
	RT	"Genetic analysis of needle proteins in maritime pine. 1. Mapping
	RT	a dominant and co-dominant protein markers assayed on diploid tissue, in
	RL	a haploid-based genetic map.";
	RN	Silvae Genetica 46:161-165(1997).
	RP	SEQUENCE.
	RC	TISSUE=Needle;
	RA	Costa P., Pionneau C., Baulw G., Dubois C., Bahrmann N., Kremer A.,
	RT	"Nucleotide sequence of the leader region of the phenylalanine operon
	RT	of <i>Escherichia coli</i> .";
	RL	Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
	RN	[2]
	RP	SEQUENCE FROM N.A.
	RX	MEDLINE=79033820; PubMed=360214;
	RA	Zurawski G., Brown K., Killingly D., Yanofsky C.;
	RT	"Nucleotide sequence of the leader region of the phenylalanine operon
	RT	of <i>Escherichia coli</i> .";
	RL	Proc. Natl. Acad. Sci. U.S.A. 75:4271-4275(1978).
	RN	[1]

Frigerio J.-M., Plomion C.;
 "Separation and characterization of needle and xylem maritime pine
 proteins";
 Electrophoresis 20:1098-1108(1999).
 -!- MISCELLANEOUS: ON THE 2D-GEL DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.5, ITS MW IS: 62 kDa.

CC ID: P81182; STANDARD: PRT; 25 AA.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

FT NON-TER 1 1
 FT NON-TER 15 15
 SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;
 [1]

Query Match 23.1%; Score 21; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1.2e+03; Indels 0; Gaps 0;
 Matches 6; Conservative 7; Mismatches 7; Gaps 0;

Qy 5 EFYLAMPATPMEA 18
 | : ||| | | |
 Db 2 BEQQIQPSATNDEA 15

RESULT 9
 ATP6_COTJA STANDARD PRT; 22 AA.
 ID P50681;
 AC P50681;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6) (FRAGMENT).
 DE MTATP6 OR ATP6.
 OS Coturnix coturnix japonica (Japanese quail).
 OG Mitochondrion.
 Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 NCBI_TaxID=93934;
 OC
 OX
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RA Ramirez V.; Morais R.;
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
 -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
 DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
 -!- SUBUNIT: F-TYPE ATPases HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CF(0)
 HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
 CC
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CC DR U36794; AAA6732.1; -.
 DR InterPro; IPR000568; -.
 DR PROSITE; PS00449; ATPASE_A; PARTIAL.
 KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
 FT NON-TER 22 22
 SQ SEQUENCE 22 AA; 2549 MW; B3E05658280D1347 CRC64;

RESULT 10
 BGBP_PENYA STANDARD PRT; 25 AA.
 ID P81182;
 AC P81182;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE BETA 1,3-D-GLUCAN BINDING PROTEIN (BGBP) (FRAGMENT).
 OS Penaeus vannamei (Penaeoidea shrimp) (European white shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostrace; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 NCBI_TaxID=6639;
 RN
 RP SEQUENCE.
 RX MEDLINE=97293426; PubMed=9149399;
 RA Vargas-Albores F.; Jimenez-Vega F.; Yepiz-Plascencia G. M.;
 RT "Purification and comparison of beta-1,3-glucan binding protein from
 white shrimp (Penaeus vannamei)." ;
 RL Comp. Biochem. Physiol. 116B:453-458(1997).
 CC -!- FUNCTION: INVOLVED IN THE RECOGNITION OF INVADING MICRO-ORGANISMS.
 CC -!- SUBUNIT: MONOMER.
 FT NON-TER 25 25
 SQ SEQUENCE 25 AA; 2743 MW; 747DD77EDC0FB06F CRC64;

Query Match 23.1%; Score 21; DB 1; Length 25;
 Best Local Similarity 44.4%; Pred. No. 2e+03; Indels 4; Mismatches 1; Gaps 0;

Qy 4 LEFYLAMPFF 12
 Db 14 LRFNMKTPP 22

RESULT 11
 CRBL_ICASP STANDARD PRT; 13 AA.
 ID CRBL_ICASP
 AC P17237;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE CHEMOTACTIC PEPTIDE (1-CP).
 OS Icaria sp. (Ropalidian wasp).
 OC Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidea; Vespidae; Polistinae; Icaria.
 NCBI_TaxID=7495;
 RN
 RP SEQUENCE.

RC TISSUE=Venom.
 RA Yasutbara T.; Itokawa H.; Suzuki N.; Nakamura H.; Nakajima T.;
 RL (In); Izumiya N. (eds.); Peptide Chemistry 1984, pp.177-182, Protein Research Foundation,
 RL Osaka (1985).
 CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
 CC OF NEUTROPHILS.
 KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
 FT MOD_RES 13 13 AMIDINATION.
 SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 22.0%; Score 20; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.5e+03; Indels 2; Mismatches 3; Gaps 0;

Qy 10 MPFATPM 16
 Db 2 VPFLGQP 8

RESULT 12

DRPH_UCAPU STANDARD; PRT; 18 AA.
 ID DRPH_UCAPU
 AC P08871;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-DEC-1988 (Rel. 37, Last annotation update)
 DE PIGMENT DISPERSING HORMONE (PDH) (LIGHT ADAPTING DISTAL RETINAL PIGMENT HORMONE) (DRPH).
 OS uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).
 OC Eumalacostraca; Arthropoda; Crustacea; Malacostraca;
 OC Subbrachyura; Eucoypodoidea; Ocyopodidae; Brachyura;
 NCBI_TaxID=6772;
 RN [1]
 RP SEQUENCE.
 RA Rao K.R., Riehm J.P., Zahnow C.A., Kleinholz L.H., Tarr G.E.,
 RA Johnson L., Norton S., Landau M., Semmes O.J., Sattelberg R.M.,
 RA Jorenby W.H., Hintz M.F.;
 RT "Characterization of a pigment-dispersing hormone in eyestalks of the fiddler crab Uca pugilator."
 RT RL PROC. NATL. ACAD. SCI. U.S.A. 82:5319-5322(1985).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=93230895; PubMed=8472537;
 RA Loehr J., Klein J., Webster S.G., Dircksen H.;
 RT "Quantification, immunoadsorbent purification and sequence analysis of a pigment-dispersing hormone of the shore crab, *Carcinus maenas* (L.).";
 RT Comp. Biochem. Physiol. 104B:699-706(1993).
 CC -!- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
 CC -!- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
 DR PIR: A25144; DRUPD.
 KW Hormone; Amidation.
 FT DOMAIN 6 9 IMPORTANT FOR DRPH ACTIVITY.
 MOD_RES 18 18 AMIDATION.
 SQ 25DSCE8DD16F544E CRC64;
 Query Match Score 20; DB 1; Length 18;
 Best Local Similarity 36.4%; Pred. No. 2.1e+03;
 Matches 4; Conservative 5; Indels 0; Gaps 0;
 Sequence 18 AA; 1928 MW;

DRPH_UCAPU STANDARD; PRT; 18 AA.
 ID DRPH_UCAPU
 AC P08871;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 37, Last sequence update)
 DT 15-DEC-1988 (Rel. 38, Last annotation update)
 DE SUPEROXIDE DISMUTASE [FE] (EC 1.15.1.1) (FRAGMENT).
 GN SODB.
 OS Pasteurella piscicida (Photobacterium damsela (subsp. *Piscicida*)).
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae;
 OC Photobacterium.
 NCBI_TaxID=38294;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=99173752; PubMed=10075430;
 RA Barnes A.C., Balebona M.C., Horne M.T., Ellis A.E.;
 RT "Superoxide dismutase and catalase in *Photobacterium damsela* subsp. *piscicida* and their roles in resistance to reactive oxygen species.";
 RT Microbiology 145:483-494(1999).
 CC -!- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -!- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: PERIPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE FAMILY.
 CC InterPro: IPR001189; -
 DR Pfam: PF00081; sodfe_1;
 RW Oxidoreductase; Iron; Periplasmic.
 FT NON-TER 20 20
 SQ SEQUENCE 20 AA; 2153 MW; A8D31FDAE8553B6D CRC64;

Query Match Score 20; DB 1; Length 20;
 Best Local Similarity 60.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 AMPFA 13
 :1:1
 Db 6 ALPYA 10

RESULT 14
 SMBP_RAT STANDARD; PRT; 25 AA.
 ID SMBP_RAT
 AC P80968;
 DT 01-NOV-1997 (Rel. 35; Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 01-NOV-1997 (Rel. 35; Last annotation update)

DE SM-1104 BINDING PROTEIN (FRAGMENTS).
 OS Ratius norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=WISTAR;
 RX MEDLINE=97407910; PubMed=9261134;
 RA Sugawara T., Matsuzaki-Fujita M., Guillaume J.-L., Camoin L.,
 RA Morooka S., Strosberg A.D.;
 RT "Characterization of a novel iodocyanopindolol and SM-11044 binding protein, which may mediate relaxation of depolarized rat colon tonus.";
 RT RL J. Biol. Chem. 272:21244-21252(1997).
 CC -!- FUNCTION: MAY MEDIATE RELAXATION OF DEPOLARIZED COLON TONUS.
 CC -!- IT BINDS IODOCYANOPINDOLOL AND SM-11044.
 CC -!- MISCELLANEOUS: THE ORDER OF THE FRAGMENTS IS UNKNOWN.

QY 1 SRLLFYFAMP 11
 Db 2 SELINSLIGLP 12

Query Match Score 20; DB 1; Length 25;
 Best Local Similarity 42.9%; Pred. No. 2.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 11 ARYFQFY 17

RESULT 15
 YIGI_SALTY STANDARD; PRT; 25 AA.
 ID YIGI_SALTY
 AC P40725;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE HYPOTHETICAL PROTEIN IN RARD-PFLA INTERGENIC REGION (FRAGMENT).
 GN YIGI.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.

OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94131966; PubMed=8300539;
RA Brok R.G.P.M., Brinkman E., van Boxtel R., Bekkers A.C.A.P.,
RA Verheij H.M., Tommassen J.;
RT "Molecular characterization of enterobacterial pldA genes encoding
RT outer membrane phospholipase A";
RL J. Bacteriol. 176:861-870(1994).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X76900; ; NOT_ANNOTATED_CDS.
DR STYGene; SG10461; Yigi.
KW Hypothetical protein.
FT NON_TER 25 25
SQ B5226164481A3CAB CRC64;
SEQUENCE 25 AA; 2827 MW;

Query Match Similarity 22.0%; Score 20; DB 1; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.9e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	6	FYLAMPF	12
Db	18	FVYHMPF	24

Search completed: May 8, 2001, 15:14:09
Job time: 530 sec

GenCore version 4.5
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[protein - protein search, using sw model]

on : May 8, 2001, 15:16:07 ; Search time 114.89 Seconds
(without alignments)
18.363 Million cell updates/sec

title: US-09-165-546A-12

perfect score: 91 sequence: 1 SRLLEPYLAMPFATPMEA 18

oring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

searched: 374700 seqs, 117207915 residues

total number of hits satisfying chosen parameters: 6627

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : SPTRIMBL_15;*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_minic:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: spUnclassified:*

13: sp_Vertebrate:*

14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query	Match	Length	DB	ID	Description
1	32	35.2	17	4	Q9UCN0		Q9ucn0 homo sapien
2	29	31.9	17	4	Q16309		Q16309 homo sapien
3	29	31.9	17	4	Q16310		Q16310 homo sapien
4	28	30.8	20	6	Q9TQX5		Q9tx5 bos taurus
5	28	30.8	24	14	O11341		O11341 molluscum o.
6	27	29.7	17	10	Q9SBY2		Q9sby2 lupinus art.
7	25	27.5	16	2	Q30985		Q30985 rhodobacter
8	25	27.5	17	2	Q9ZG33		Q9zg33 chlamydia t.
9	25	27.5	24	4	Q96346		Q96346 brassica na
10	24.5	26.9	23	4	Q16884		Q16884 homo sapien
11	24	26.4	15	2	Q9R5A0		Q9r5a0 micrococcus
12	24	26.4	20	2	Q9R896		Q9r896 chlamydia t.
13	24	26.4	20	6	Q9TR72		Q9tr72 ursus arcto
14	24	26.4	21	2	Q9S1C0		Q9s1c0 porphyromon
15	24	26.4	23	11	Q9R231		Q9r231 rattus norve
16	24	26.4	25	10	Q94983		Q94983 lycopersicum
17	24	26.4	25	11	Q9OQ72		Q9quz2 mus sp. 50-
18	23.5	25.8	26	8	Q95475		Q95475 sacharomy
19	23	25.3	16	14	Q79458		Q79458 human immun

20	25.3	18	2	Q9ZG42 chlamydia t
21	25.3	18	4	Q9UCF9 homo sapien
22	25.3	20	10	Q9S8X5 glycine max
23	25.3	20	11	Q9QB9 ratmus sp.
24	25.3	23	11	Q9Z208 mus musculu
25	25.3	24	2	Q9T4Q6 amycolatops
26	25.3	24	14	Q96628 bovinus aden
27	25.3	24	14	Q69137 human herpe
28	24.2	11	2	Q9R7U8 pseudomonas
29	22	16	10	Q9SPV1 nicotiana t
30	22	24.2	17	Q19716 homosapien
31	22	24.2	18	Q9TRG2 orctocelus
32	22	24.2	19	Q44506 anabaena va
33	22	24.2	20	Q47598 escherichia
34	22	24.2	20	P79256 atotus trivi
35	22	24.2	21	Q53014 rhizobium e
36	22	24.2	21	Q9TRC5 canis famili
37	22	24.2	22	Q9WY1 drosophila
38	22	24.2	22	Q93389 ovis aries
39	22	24.2	22	Q87084 pseudorabie
40	22	24.2	23	Q68983 pseudorabie
41	22	24.2	23	Q68391 pseudorabie
42	22	24.2	23	Q63392 pseudorabie
43	22	24.2	23	Q63193 pseudorabie
44	22	24.2	23	Q87078 pseudorabie
45	22	24.2	23	Q87079 pseudorabie

ALIGNMENTS

```

RESULT 1
Q9UCNO PRELIMINARY; PRT; 17 AA.
ID Q9UCNO;
AC Q9UCNO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TRANSFERRIN RECEPTOR.
OS Homo sapiens (Human).
OC Bivalvia: Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia: Rutheria; Primates; Catarrini; Hominiidae; HOMO;
NCBI_TaxId=9606;
OX

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RESULT		2			
Q16309	ID	Q16309	PRELIMINARY;	PRT;	17 AA.
AC	AC	Q16309;			
DT	DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	DT	01-MAY-1999	(TREMBLrel. 09, Last sequence update)		
DT	DT	01-MAY-1999	(TREMBLrel. 10, Last annotation update)		
DE	GC*IF PROTEIN (FRAGMENT).				
GN	OS				
	Homo sapiens (Human).				
	GC*IF.				

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RP SEQUENCE.
RP MEDLINE=92375195; PubMed=1380674;
RX Chicz R.M., Urban R.G., Lane W.S., Gorga J.C., Stern L.J.,
RA Strominger J.L., Vignali D.A.

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OX	NCBI_TaxID=9913;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OX	[1]
OX	MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO;	RN	SEQUENCE
[1]	SEQUENCE FROM N.A.; PubMed=7725672;	RP	
RX	MEDLINE=95242701; PubMed=7725672;	RX	PUBMED-8980530;
RX	Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;	RA	MEDLINE=97135072; PubMed=8980530;
RA	"Characterization of mutants of the vitamin-D-binding protein/group	RA	He N.G., Singhal S.S., Chaubey M., Awasthi S., Zimniak P.,
RT	specific component: GC aborigine (1A1) from Australian aborigines and	RA	Partridge C.A., Awasthi Y.C.;
RT	South African blacks, and 2A9 from south Germany.";	RT	"Purification and characterization of a 4-hydroxyxenonental metabolizing
RT	Vox Sang 68:50-54(1995);	RT	glutathione S-transferase isozyme from bovine pulmonary microvessel
RL	EMBL; S77129; AAD14249.1;	RT	endothelial cells.";
DR	NON_TER 17 17 BB2982750293722C CRC64;	RL	Biochim Biophys Acta 1291:182-188(1996).
SQ	SEQUENCE 17 AA; 1852 MW;	SEQUENCE 20 AA; 2292 MW; 12BA99647E94AB0 CRC64;	
Query Match	Score 29; DB 4; Length 17;	Query Match	Score 30 8%; DB 6; Length 20;
Best Local Similarity	75.0%;	Best Local Similarity	71.4%;
Matches	Pred. No. 2.2e+02; 0; Mismatches 2;	Matches	Pred. No. 3.9e+02; 0; Mismatches 2;
QY	10 MPFATPME 17	QY	11 PFATPME 17
Db	1 MPDATPTE 8	Db	5 PFKTPKE 11
RESULT	5	RESULT	5
ID	Q16310	ID	Q11341
AC	Q16310_	AC	Q11341_
CD	PRELIMINARY;	CD	PRELIMINARY;
DT	01-NOV-1996 (TREMBLrel. 01, Created)	DT	01-JUL-1997 (TREMBLrel. 04, Created)
DT	01-JAN-1999 (TREMBLrel. 09, Last sequence update)	DT	01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)	DE	SIMILAR TO VARIOLA FIR AND VACCINA DIR (FRAGMENT).
DE	GC*2 PROTEIN (FRAGMENT).	GN	BI-14-1.
GN	Homo sapiens (Human).	OS	Molluscum contagiosum virus subtype 1 (MCV1).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC	MAMMALIA; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC	Moniliophytoviruses
OX	MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO;	OX	NCBI_TaxID=10280;
RN	SEQUENCE FROM N.A.; PubMed=7725672;	RN	SEQUENCE FROM N.A.
RX	Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;	RA	Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J., Lopez-Estebaranz J.L., Estebaran M., Martin-Gallardo A.;
RA	"Characterization of mutants of the vitamin-D-binding protein/group	RA	SEQUENCE FROM N.A.
RT	specific component: GC aborigine (1A1) from Australian aborigines and	RA	Virus Genes 0-0-0(O).
RT	South African blacks, and 2A9 from south Germany.";	DR	EMBL; U86918; AAB57974.1; -.
RT	Vox Sang 68:50-54(1995);	FT	NON_TER 1 1
RL	EMBL; S77130; AAD14250.1; -.	SEQUENCE	24 AA; 2892 MW; 6052DD2609CAFAD0 CRC64;
FT	NON_TER 17 17 BB26CAD60293722C CRC64;	Query Match	Score 30 8%; DB 14; Length 24;
SQ	SEQUENCE 17 AA; 1845 MW;	Best Local Similarity	45.5%; Pred. No. 4.6e+02; 3; Mismatches 3;
QY	10 MPFATPME 17	Matches	Indels 0; Gaps 0; Gaps 0;
Db	1 MPDATPTE 8	Db	12 LLQYYVYYVFA 22
RESULT	6	RESULT	6
ID	Q9TQX5	ID	Q9SBY2
AC	Q9TQX5_	AC	Q9SBY2_
CD	PRELIMINARY;	CD	PRELIMINARY;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	L-ASPARAGINASE ISOFORM A (EC 3.5.1.1).	DE	L-ASPARAGINASE ISOFORM A (EC 3.5.1.1).
OS	Lupinus arboreus (tree lupine).	OS	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I;	OC	Fabales; Fabaceae; Papilionoideae; Lupinus.
OC	Bovidae; Bovinae; Bos.	OX	NCBI_TaxID=3872;
RN	SEQUENCE 17 AA; 1877 MW;	RN	DB7925924D5F46AF CRC64;
RP	SEQUENCE	RP	
RA	Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H., Faridjen K.J.;	RA	
RA	Phytochemistry 31:1519-1527 (1992)	RL	
SQ	SEQUENCE 17 AA;	SQ	DB7925924D5F46AF CRC64;

RT "Identification of the start sites for the 1.9- and 1.4-kb rat
RT transforming growth factor- β transcripts and their effect on
RT translational efficiency.";
RL Gene 219:81-89(1998).
DR EMBL; AF105069; AAD20222.1;
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2550 MW; 26AA10E5D88B68F4 CRC64;

Query Match 26.4%; Score 24; DB 11; Length 23;
Best Local Similarity 45.5%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 RLLEPYLAMPF 12
| || | :|:
Db 7 RLPLPLPLPW 17

Search completed: May 8, 2001, 15:16:08
Job time: 534 sec

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OM protein - protein search, using sw model

Run on: May 8, 2001, 15:05:14 ; Search time 62.11 Seconds
(without alignments)
5.567 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNLTIRLTAADHQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters : 110741

Minimum DB seq length: 0
Maximum DB seq length: 25

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn1_6/p todada/2/iaa/5A-COMB.pep:
2: /cgn2_6/p todada/2/iaa/5B-COMB.pep:
3: /cgn12_6/p todada/2/iaa/6A-COMB.pep:
4: /cgn2_6/p todada/2/iaa/6B-COMB.pep:
5: /cgn1_6/p todada/2/iaa/5ETUS-COMB.pep:
6: /cgn12_6/p todada/2/iaa/backfiles1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal 1 to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	35.2	25	1 US-09-087-772A-8	Sequence 8, Appli Patent No. 5185441
2	29	33.0	17	6 5185441-3	Sequence 123, APP
3	29	33.0	23	1 US-08-036-555B-123	Sequence 123, APP
4	29	33.0	23	1 US-08-469-569-123	Sequence 123, APP
5	29	33.0	23	1 US-08-249-522A-123	Sequence 123, APP
6	29	33.0	23	1 US-08-469-526A-123	Sequence 123, APP
7	29	33.0	23	1 US-08-734-591A-123	Sequence 123, APP
8	29	33.0	23	2 US-08-469-660-123	Sequence 123, APP
9	29	33.0	23	4 US-08-335-123	Sequence 123, APP
10	29	33.0	23	4 US-08-735-021-123	Sequence 123, APP
11	29	33.0	23	4 US-08-734-664A-123	Sequence 123, APP
12	29	33.0	23	5 PCT-US94-05083C-119	Sequence 119, APP
13	29	33.0	23	5 PCT-US95-06846A-123	Sequence 123, APP
14	29	33.0	24	3 US-08-460-576-7	Sequence 7, Appli
15	28	33.0	25	1 US-08-029-402-5	Sequence 5, Appli
16	28	31.8	21	1 US-07-593-657-1	Sequence 1, Appli
17	27	30.7	25	2 US-08-726-306A-67	Sequence 67, Appli
18	26	29.5	16	1 US-08-036-555B-121	Sequence 121, APP
19	26	29.5	16	1 US-08-469-569-121	Sequence 121, APP
20	26	29.5	16	1 US-08-249-522A-121	Sequence 121, APP
21	26	29.5	16	1 US-08-469-526A-121	Sequence 121, APP
22	26	29.5	16	2 US-08-734-591A-121	Sequence 121, APP
23	26	29.5	16	2 US-08-469-660-121	Sequence 121, APP
24	26	29.5	16	4 US-08-470-335-121	Sequence 121, APP
25	26	29.5	16	4 US-08-735-021-121	Sequence 121, APP
26	26	29.5	16	4 US-08-734-664A-121	Sequence 121, APP
27	26	29.5	16	5 PCT-US94-05083C-117	Sequence 117, APP

Qy 1 TVSGNLT 9
|| || |

RESULT 1
US-08-087-772A-8
; Sequence 8, Application US/08087772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Nahmias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine Beta3-Adrenergic Receptor and Their Applications
; TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 28234
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087-772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 33339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-087-772A-8

ALIGNMENTS

28	26	29.5	16	5 PCT-US95-06846A-121	Sequence 121, APP
29	26	29.5	18	2 US-08-702-105A-15	Sequence 15, APP
30	26	29.5	18	3 US-08-702-110A-15	Sequence 15, APP
31	25	28.4	9	4 US-09-258-754-53	Sequence 253, APP
32	25	28.4	11	1 US-08-665-966-4	Sequence 4, APP
33	25	28.4	11	3 US-09-041-780-4	Sequence 4, APP
34	25	28.4	19	1 US-08-466-033-79	Sequence 79, APP
35	25	28.4	19	2 US-08-444-733-9	Sequence 79, APP
36	25	28.4	19	2 US-08-464-134-79	Sequence 79, APP
37	25	28.4	19	2 US-08-461-361-79	Sequence 79, APP
38	25	28.4	19	2 US-08-485-910-79	Sequence 79, APP
39	25	28.4	19	5 PCT-US95-0666-63	Sequence 63, APP
40	25	28.4	20	1 US-08-289-653-3	Sequence 63, APP
41	25	28.4	20	1 US-08-318-193-3	Sequence 63, APP
42	25	28.4	20	1 US-08-385-16-10	Sequence 10, APP
43	25	28.4	20	4 US-09-230-421-11	Sequence 11, APP
44	25	28.4	21	2 US-08-283-74	Sequence 24, APP
45	25	28.4	21	2 US-08-746-257A-22	Sequence 22, APP

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Db 13 TVGGNLLV1 21

RESULT 2
; Patent No. 518541-3
; APPLICANT: WALLNER, BARBARA P.; HESSIENS, CATHERINE
; TITLE OF INVENTION: DNA SEQUENCES, RECOMBINANT DNA
; MOLECULES AND PROCESSES FOR PRODUCING PI-LINKED LYMPHOCYTE
; FUNCTION ASSOCIATED ANTIGEN-3
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/237,309
; SEQ ID NO:3;
; FILING DATE: 26-AUG-1988
; LENGTH: 17
; 518541-3

Query Match 33.0%; Score 29; DB 6; Length 17;
Best Local Similarity 46.28%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

RESULT 3
US-08-036-555B-123
Sequence 123, Application US/08036555B
; Patent No. 5530109
GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; ADDRESS: Feife & Lynch
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; CORRESPONDENCE ADDRESS:
; ADDRESS: Feife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/963,703
; FILING DATE: 03-APRIL-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-036-555B-123

Query Match 33.0%; Score 29; DB 1; Length 23;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ILLITIRTAADH 16
; Sequence 123, Application US/08469569
; Patent No. 5606032
GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; ADDRESS: Feife & Lynch
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884

```

INFORMATION FOR SEQ ID NO: 123:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-469-569-123

Query Match	Score 29;	DB 1;	Length 23;
Best Local Similarity	53.0%	Pred. No. 47;	
Matches	6;	Mismatches	0;
Qy	6 ILTIRTAADH 16		
	:1:1:1 1		
Db	1 LLTVRLGANGH 11		

RESULT 5
 US-08-249-322A-123
 Sequence 123, Application US/08249322A
 Patent No. 5/16930

GENERAL INFORMATION:
 APPLICANT: Goodearl, Andrew; Stroobant, Paul;
 MINGHETTI, Luisa; Waterfield, Michael;
 Marchionni, Mark;
 APPLICANT: Chen, Maio Su; Hiles, Ian
 TITLE OF INVENTION: Glial Mitogenic Factors, Their
 Preparation and Use
 NUMBER OF SEQUENCES: 184
 CORRESPONDENCE ADDRESS:
 ADDRESS: Feife & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022

COMPUTER READABLE FORM:
 COMPUTER: IBM
 COMPUTER SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/249,322A
 FILING DATE: 26-MAY-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/036,555
 FILING DATE: 24-MAR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/955,173
 FILING DATE: 23-OCT-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/940,389
 FILING DATE: 03-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/907,138
 FILING DATE: 30-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/863,703
 FILING DATE: 03-APRIL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsai, Christine H.
 REGISTRATION NUMBER: 34,266
 REFERENCE/DOCKET NUMBER: LUD 250.4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-3884
 TELEFAX: (212) 838-3884
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-469-526A-123

Query Match

Score 29;	DB 1;	Length 23;	
Best Local Similarity	54.5%;	Pred. No. 47;	
Matches	6;	Mismatches	2;
Qy	6 ILTIRTAADH 16		
	:1:1:1 1		
Db	1 LLTVRLGANGH 11		

RESULT 6
 US-08-469-526A-123
 Sequence 123, Application US/08469526A
 Patent No. 5/79249

GENERAL INFORMATION:
 APPLICANT: Goodearl, Andrew
 MINGHETTI, Luisa
 WATERFIELD, Michael
 MARCIONNI, Mark
 CHEN, Maio Su
 HILES, Ian
 TITLE OF INVENTION: Glial Mitogenic Factors, Their
 Preparation and Use
 NUMBER OF SEQUENCES: 187
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 176 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,526A
 FILING DATE: 06-JUNE-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/036,555
 FILING DATE: 24-MAR-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/955,173
 FILING DATE: 23-OCT-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/940,389
 FILING DATE: 03-SEP-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/907,138
 FILING DATE: 03-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/863,703
 FILING DATE: 03-APRIL-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: U.K. 91 07566.3
 FILING DATE: 10-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Blieker-Trady, Kristina
 REGISTRATION NUMBER: 39,109
 REFERENCE/DOCKET NUMBER: 04585/00200A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-428-0200
 TELEFAX: 617-428-7045
 INFORMATION FOR SEQ ID NO: 123:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-469-526A-123

Query Match Score 29; DB 1; Length 23;
 Best Local Similarity 54.5%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

LENGTH: 23
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-734-591A-123

RESULT 7
 US 08-734-591A-123
 Sequence 123, Application US/08734591A
 Patent No. 5854220

GENERAL INFORMATION:
 APPLICANT: Goodearl, Andrew
 APPLICANT: Stroobant, Paul
 APPLICANT: Minghetti, Luisa
 APPLICANT: Waterfield, Michael
 APPLICANT: Hiles, Ian
 APPLICANT: Marchionni, Mark
 APPLICANT: Chen, Mario
 TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR PREPARATION AND USE
 TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION, THEIR PREPARATION AND USE
 NUMBER OF SEQUENCES: 187
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 176 Federal Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible Pentium
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Wordperfect (Version 7.0)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/734,591A
 FILING DATE: 22-OCT-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/470,335
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/036,555
 FILING DATE: 03-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/965,173
 FILING DATE: 23-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/940,389
 FILING DATE: 03-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/907,138
 FILING DATE: 30-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/863,703
 FILING DATE: 03-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 91 07566.3
 FILING DATE: 10-APR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Bleier Brady, Kristina
 REGISTRATION NUMBER: 39,109
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 428-0200
 TELEX: (617) 428-7045
 INFORMATION FOR SEQ ID NO: 123:
 SEQUENCE CHARACTERISTICS:

LENGTH: 23
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-469-660-123

RESULT 8
 US 08-469-660-123
 Sequence 123, Application US/08469660

GENERAL INFORMATION:
 APPLICANT: Gwynne, David I.; Marchionni, Mark;
 APPLICANT: McBurney, Robert N.
 TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
 TITLE OF INVENTION: THEIR PREPARATION AND USE
 NUMBER OF SEQUENCES: 184
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 ZIP: 02111-3804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,660

FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/011,396
 FILING DATE: 29-JAN-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/984,085
 FILING DATE: 01-DEC-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/011,396
 FILING DATE: 29-JAN-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/927,337
 FILING DATE: 10-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 04585/017004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: 200154
 INFORMATION FOR SEQ ID NO: 123:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-469-660-123

Query Match Score 29; DB 2; Length 23;
 Best Local Similarity 54.5%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 9
 Qy 6 ILTIRLTAADH 16
 ; SEQ ID NO: 123
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-08-470-335-123
 ; Sequence 123, Application US/08470335F
 ; Patent No. 6147150
 ; GENERAL INFORMATION:
 ; APPLICANT: GOODEARL, ANDREW
 ; APPLICANT: STROOBANT, PAUL
 ; APPLICANT: MINGHETTI, LUISA
 ; APPLICANT: WATERFIELD, MICHAEL
 ; APPLICANT: MARCHIONNI, MARK
 ; APPLICANT: HILES, IAN S.
 ; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
 ; TITLE OF INVENTION: PREPARATION AND USE
 ; FILE REFERENCE: 04585/00200B
 ; CURRENT APPLICATION NUMBER: US/08/470,335F
 ; CURRENT FILING DATE: 1995-06-06
 ; EARLIER APPLICATION NUMBER: 08/036,555
 ; EARLIER FILING DATE: 1993-03-24
 ; NUMBER SEQ ID NOS: 252
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 123
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-08-470-335-123

Query Match 33.0%; Score 29; DB 4; Length 23;
 Best Local Similarity 54.5%; Pred. No. 47;
 Matches 6; Conservative 3; Indels 0; Gaps 0;

RESULT 10
 Qy 6 ILTIRLTAADH 16
 ; SEQ ID NO: 123
 ; Sequence 123, Application US/08735021B
 ; Patent No. 6194377
 ; GENERAL INFORMATION:
 ; APPLICANT: GOODEARL, ANDREW
 ; APPLICANT: STROOBANT, PAUL
 ; APPLICANT: MINGHETTI, LUISA
 ; APPLICANT: WATERFIELD, MICHAEL
 ; APPLICANT: MARCHIONNI, MARK
 ; APPLICANT: HILES, IAN S.
 ; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
 ; TITLE OF INVENTION: PREPARATION AND USE
 ; FILE REFERENCE: 04585/00200B
 ; CURRENT APPLICATION NUMBER: US/08/735,021B
 ; CURRENT FILING DATE: 1996-10-22
 ; EARLIER APPLICATION NUMBER: 08/472,065
 ; EARLIER FILING DATE: 1995-06-06
 ; EARLIER APPLICATION NUMBER: 08/036,555
 ; EARLIER FILING DATE: 1993-03-24
 ; EARLIER APPLICATION NUMBER: 07/965,173
 ; EARLIER FILING DATE: 1992-10-23
 ; EARLIER APPLICATION NUMBER: 07/940,389
 ; EARLIER FILING DATE: 1992-09-03
 ; EARLIER APPLICATION NUMBER: 07/907,138
 ; EARLIER FILING DATE: 1992-06-30
 ; EARLIER APPLICATION NUMBER: 07/863,703
 ; EARLIER FILING DATE: 1992-04-03
 ; NUMBER SEQ ID NOS: 192
 ; SOFTWARE: FastSEQ for Windows Version 3.0

RESULT 11
 Qy 6 ILTIRLTAADH 16
 ; SEQ ID NO: 123
 ; LENGTH: 23;
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-08-735-021-123
 ; Sequence 123, Application US/08734664A
 ; Patent No. 6204241
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodearl, Andrew
 ; APPLICANT: Stroobant, Paul
 ; APPLICANT: Minghetti, Luisa
 ; APPLICANT: Waterfield, Michael
 ; APPLICANT: Marchionni, Mark
 ; APPLICANT: Chen, Mario
 ; APPLICANT: Hiles, Ian
 ; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
 ; TITLE OF INVENTION: PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 187
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Clark & Elbing LLP
 ; STREET: 176 Federal Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette 1.44 Mb
 ; COMPUTER: IBM Compatible Pentium
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/734,664A
 ; FILING DATE: 22-OCT-1996
 ; CLASSIFICATION: 536
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249,322
 ; FILING DATE: 26-MAY-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/036,555
 ; FILING DATE: 24-MAR-1993
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/965,173
 ; FILING DATE: 23-OCT-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/940,389
 ; FILING DATE: 03-SEP-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/907,138
 ; FILING DATE: 30-JUN-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/863,703
 ; FILING DATE: 03-APR-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: UK 91 07566.3
 ; FILING DATE: 10-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bieker-Brady, Kristina
 ; REGISTRATION NUMBER: 39,109
 ; REFERENCE/DOCKET NUMBER: 04585/00200J
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 428-0200
 TELEFAX: (617) 428-7045
 TELEX: 1 LLTIRLAAZH 11

SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-734-664A-123

RESULT 1.3
 PCT-US95-06846A-123
 Sequence 123, Application PC/US9506846A
 GENERAL INFORMATION:
 APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
 MANGHETTI, Luisa; Waterfield, Michael; Marchioni, Mark;
 APPLICANT: Chen, Mai; Hiles, Ian
 TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use
 NUMBER OF SEQUENCES: 178
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06846A
 FILING DATE: 25-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,322
 FILING DATE: 26-MAY-1994
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/036,555
 FILING DATE: 24-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/965,173
 FILING DATE: 23-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/940,389
 FILING DATE: 03-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/907,138
 FILING DATE: 30-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/863,703
 FILING DATE: 03-APRIL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.K. 91 07566.3
 FILING DATE: 10-APRIL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, Norman D.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: LUD 5250.5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 119:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 PCT-US94-05083C-119

Qy 6 ILTIRLAAZH 16
 :1:1:1:1:1:1
 Db 1 LLTIRLAAZH 11

Query Match 33.0% ; Score 29; DB 5; Length 23;
 Best Local Similarity 54.5%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 ILTIRLAAZH 16
 :1:1:1:1:1:1
 Db 1 LLTIRLAAZH 11

Query Match 33.0% ; Score 29; DB 5; Length 23;
 Best Local Similarity 54.5%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db    :||:|| 1 LITVRLGAWH 11
      ; ZIP: 20036
      ; COMPUTER READABLE FORM:
      ; MEDIUM TYPE: Floppy disk
      ; COMPUTER: IBM PC compatible
      ; OPERATING SYSTEM: PC-DOS/MS-DOS
      ; SOFTWARE: PatentIn Release #1.0, Version #1.25
      ; CURRENT APPLICATION DATA:
      ; APPLICATION NUMBER: US/08/029,402
      ; FILING DATE: 19930305
      ; CLASSIFICATION: 435
      ; ATTORNEY/AGENT INFORMATION:
      ; NAME: FOX, Samuel L.
      ; REGISTRATION NUMBER: 30,353
      ; REFERENCE/DOCKET NUMBER: 0614.0860001
      ; TELECOMMUNICATION INFORMATION:
      ; TELEPHONE: (202) 466-0800
      ; TELEFAX: (202) 833-8716
      ; INFORMATION FOR SEQ ID NO: 5:
      ; SEQUENCE CHARACTERISTICS:
      ; LENGTH: 25 amino acids
      ; TYPE: AMINO ACID
      ; TOPOLOGY: linear
      ; MOLECULE TYPE: protein
      ; US-08-029-402-5

Query Match          Score 29; DB 1; Length 25;
Best Local Similarity 46.7%; Pred No. 52;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY  2 VSGNLTIRLTAADH 16
  || :|| :|| | |
  2 VSATVLYLAAAH 16

Search completed: May 8, 2001, 15:05:15
Job time: 111 sec

      ; INFORMATION FOR SEQ ID NO: 7:
      ; SEQUENCE CHARACTERISTICS:
      ; LENGTH: 24 amino acids
      ; TYPE: amino acid
      ; STRANDEDNESS: single
      ; TOPOLOGY: linear
      ; MOLECULE TYPE: peptide
      ; US-08-460-576-7

Query Match          Score 29; DB 3; Length 24;
Best Local Similarity 46.7%; Pred No. 49;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY  2 VSGNLTIRLTAADH 16
  || :|| :|| | |
  2 VSATVLYLAAAH 16

RESULT 15
US-08-029-402-5
; Sequence 5, Application US/08029402
; General Information:
; Applicant: Murphy, Cheryl I.
; Applicant: Young, Elihu
; Title of Invention: Baculovirus Vectors For Expression of
; Title of Invention: Secretory and Membrane-Bound Proteins
; Number of Sequences: 19
; Correspondence Address:
; Addressee: Sterne, Kessler, Goldstein & Fox
; Street: 1225 Connecticut Avenue
; City: Washington
; State: D.C.
; Country: U.S.A.

```


Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	DCMS_PSECF
Gapop:	10.0 , Gapext:	0.5	35	18	20.5	20	1	Pseudomonas
Searched:	93435 seqs, 34255486 residues	Total number of hits satisfying chosen parameters:	1423	36	18	20.5	23	P29188 rattus norv
Minimum DB seq length:	0	ID:	CHP_THICU	37	18	20.5	25	P30551 heliothis v
Maximum DB seq length:	25	ID:	P80486;	38	17	19.3	10	P28807 spinacia ol
Post-processing:	Minimum Match 0%	AC:	DT	39	17	19.3	15	P41494 dirosophila
	Maximum Match 100%	DT	40	17	19.3	15	P81085 pinus pinas	
Database :	SwissProt_39;*	DE:	41	17	19.3	15	P21586 caretta car	
Scoring table:	BLOSUM62	Score:	42	17	19.3	15	P81082 pinus pinas	
Gapop:	10.0 , Gapext:	0.5	43	17	19.3	16	P80563 pelobacter	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Total:	44	17	19.3	17	P36530 saccharomy	
Perfect score:	88	Score:	45	17	19.3	17	O9zziu5 salmonella	
Title:	US-09-165-546A-13	Length:	45	17	19.3	19	P82030 uperoleia i	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P19915 pseudomonas
Gapop:	10.0 , Gapext:	0.5	35	18	20.5	20	1	P29188 rattus norv
Searched:	93435 seqs, 34255486 residues	Total:	36	18	20.5	23	1	PAP1_HELVI
Minimum DB seq length:	0	ID:	CHP_THICU	37	18	20.5	25	1
Maximum DB seq length:	25	ID:	P80486;	38	17	19.3	10	1
Post-processing:	Minimum Match 0%	AC:	DT	39	17	19.3	15	1
	Maximum Match 100%	DT	40	17	19.3	15	1	
Database :	SwissProt_39;*	DE:	41	17	19.3	15	1	
Scoring table:	BLOSUM62	Score:	42	17	19.3	16	1	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	1	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	1	
Perfect score:	88	Length:	45	17	19.3	19	1	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	1	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	DCMS_PSECF
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P29188 rattus norv
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P30551 heliothis v
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	P28807 spinacia ol
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P41494 dirosophila
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P81085 pinus pinas	
	Maximum Match 100%	DT	40	17	19.3	15	P21586 caretta car	
Database :	SwissProt_39;*	DE:	41	17	19.3	15	P81082 pinus pinas	
Scoring table:	BLOSUM62	Score:	42	17	19.3	16	P80563 pelobacter	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P36530 saccharomy	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	O9zziu5 salmonella	
Perfect score:	88	Length:	45	17	19.3	19	P82030 uperoleia i	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P19915 pseudomonas	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P29188 rattus norv
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P30551 heliothis v
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P28807 spinacia ol
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	P41494 dirosophila
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P81085 pinus pinas
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P21586 caretta car	
	Maximum Match 100%	DT	40	17	19.3	15	P81082 pinus pinas	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P80563 pelobacter	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P36530 saccharomy	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	O9zziu5 salmonella	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P82030 uperoleia i	
Perfect score:	88	Length:	45	17	19.3	19	P19915 pseudomonas	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P29188 rattus norv	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P30551 heliothis v
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P28807 spinacia ol
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P41494 dirosophila
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	P81085 pinus pinas
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P21586 caretta car
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P81082 pinus pinas	
	Maximum Match 100%	DT	40	17	19.3	15	P80563 pelobacter	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P36530 saccharomy	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	O9zziu5 salmonella	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P82030 uperoleia i	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P19915 pseudomonas	
Perfect score:	88	Length:	45	17	19.3	19	P29188 rattus norv	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P30551 heliothis v	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P28807 spinacia ol
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P41494 dirosophila
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P81085 pinus pinas
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	P21586 caretta car
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P81082 pinus pinas
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P80563 pelobacter	
	Maximum Match 100%	DT	40	17	19.3	15	P36530 saccharomy	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	O9zziu5 salmonella	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P82030 uperoleia i	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P19915 pseudomonas	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P29188 rattus norv	
Perfect score:	88	Length:	45	17	19.3	19	P30551 heliothis v	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P28807 spinacia ol	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P41494 dirosophila
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P81085 pinus pinas
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P21586 caretta car
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	P80563 pelobacter
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P36530 saccharomy
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	O9zziu5 salmonella	
	Maximum Match 100%	DT	40	17	19.3	15	P82030 uperoleia i	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P19915 pseudomonas	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P29188 rattus norv	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P30551 heliothis v	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P28807 spinacia ol	
Perfect score:	88	Length:	45	17	19.3	19	P41494 dirosophila	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P81085 pinus pinas	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P21586 caretta car
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P80563 pelobacter
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P36530 saccharomy
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	O9zziu5 salmonella
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P82030 uperoleia i
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P19915 pseudomonas	
	Maximum Match 100%	DT	40	17	19.3	15	P29188 rattus norv	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P30551 heliothis v	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P28807 spinacia ol	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P41494 dirosophila	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P81085 pinus pinas	
Perfect score:	88	Length:	45	17	19.3	19	P21586 caretta car	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P28807 spinacia ol	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P21586 caretta car
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P80563 pelobacter
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P36530 saccharomy
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	O9zziu5 salmonella
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P82030 uperoleia i
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P19915 pseudomonas	
	Maximum Match 100%	DT	40	17	19.3	15	P29188 rattus norv	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P30551 heliothis v	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P28807 spinacia ol	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P41494 dirosophila	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P81085 pinus pinas	
Perfect score:	88	Length:	45	17	19.3	19	P21586 caretta car	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P28807 spinacia ol	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P21586 caretta car
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P80563 pelobacter
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P36530 saccharomy
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	O9zziu5 salmonella
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P82030 uperoleia i
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P19915 pseudomonas	
	Maximum Match 100%	DT	40	17	19.3	15	P29188 rattus norv	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P30551 heliothis v	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P28807 spinacia ol	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P41494 dirosophila	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P81085 pinus pinas	
Perfect score:	88	Length:	45	17	19.3	19	P21586 caretta car	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P28807 spinacia ol	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P21586 caretta car
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P80563 pelobacter
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P36530 saccharomy
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	O9zziu5 salmonella
Maximum DB seq length:	25	AC:	DT	38	17	19.3	10	P82030 uperoleia i
Post-processing:	Minimum Match 0%	DT	39	17	19.3	15	P19915 pseudomonas	
	Maximum Match 100%	DT	40	17	19.3	15	P29188 rattus norv	
Database :	SwissProt_39;*	DE:	41	17	19.3	16	P30551 heliothis v	
Scoring table:	BLOSUM62	Score:	42	17	19.3	17	P28807 spinacia ol	
Gapop:	10.0 , Gapext:	Total:	43	17	19.3	17	P41494 dirosophila	
Sequence:	1 TVSGNLTIRLTAADHQ 18	Score:	44	17	19.3	17	P81085 pinus pinas	
Perfect score:	88	Length:	45	17	19.3	19	P21586 caretta car	
Title:	US-09-165-546A-13	Score:	45	17	19.3	19	P28807 spinacia ol	
Scoring table:	BLOSUM62	Score:	34	18	20.5	20	1	P21586 caretta car
Gapop:	10.0 , Gapext:	Total:	35	18	20.5	20	1	P80563 pelobacter
Searched:	93435 seqs, 34255486 residues	ID:	CHP_THICU	36	18	20.5	23	P36530 saccharomy
Minimum DB seq length:	0	ID:	P80486;	37	18	20.5	25	O9zziu5 salmonella

RA Burland V.D.; Plunkett G. III; Daniels D.L.; Blattner F.R.;
 RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
 genome: organizational symmetry around the origin of replication.";
 RT Genomics 16:1551-561(1993).

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CC DR EMBL; M11980; AAA24678.1; -.
 DR EMBL; L10328; AAA62058.1; -.
 DR EMBL; AE000448; AAC76730.1; -.
 DR ECOgene; EG11276; thal.
 KW Leader Peptide.
 SQ SEQUENCE 24 AA; 2894 MW; 66E3987EA7C052F9 CRC64;

Query Match 27.8%; Score 24.5; DB 1; Length 24;
 Best Local Similarity 36.4%; Pred. No. 3.4e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 9; Gaps 1;

Qy 5 NLTIRUTA-----ADHR 17
 ||| | :|||
 Db 2 NILHICVTSKWNIDNKRIVDHR 23

RESULT 3
 DCML_PSECA ID DCML_PSECA STANDARD; PRT; 12 AA.
 AC P19919;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CARBON MONOXIDE OXYGENASE [CYTOCHROME B-561] LARGE CHAIN (EC 1.2.2.4)
 DE (FRAGMENT).
 OS Pseudomonas carboxydovorans.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group; Oligotropha.
 OC NCBI_TaxID=40137;
 RN [1]
 RP SEQUENCE.

RC STRAIN=OM5; PubMed=2818128;
 RX Kraut M., Hugendieck T., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 carboxydrophic bacteria";
 RT Arch. Microbiol. 152:335-341 (1989).
 RL 2 H(+)+ FERRICYTOCHROME B-561.
 CC -!- COFACTOR: MOLYBDENUM.
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; PL0138; PLO138.

KW Oxidoreductase; Molybdenum.
 FT VARIANT 11 12 GE -> EK.
 FT NON_TER 12 12 SQ SEQUENCE 12 AA; 1289 MW; 9B170C688E6B02D1 CRC64;

Query Match 27.3%; Score 24; DB 1; Length 12;
 Best Local Similarity 45.5%; Pred. No. 2e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 NLTIRUTAAD 15
 ||| :|||:
 Db 2 NIQTQVEPTAGE 12

RESULT 4

PSBF_SYNNU ID PSBF_SYNNU STANDARD; PRT; 21 AA.
 AC P1239;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 CC CYTOCHROME B559 BETA CHAIN (FRAGMENT).
 DE GN PSBF.
 OS Synochococcus vulcanus.
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OC NCBI_TaxID=32053;
 RN
 RP SEQUENCE.
 RA Ikeyachi M., Koike H., Inoue Y.;
 RT "Identification of psbf and psbl gene products in cyanobacteria
 photosystem II reaction center preparation.,";
 RL FEBS Lett. 251:155-160(1989).
 CC -!- FUNCTION: THIS B-TYPE CYTOCHROME IS TIGHTLY ASSOCIATED WITH THE
 CC REACTION CENTER OF PHOTOSYSTEM II AND POSSIBLY IS PART OF THE
 CC WATER-OXIDATION COMPLEX.
 CC -!- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.
 CC -!- SIMILARITY: BELONGS TO THE PSBE / PSBF FAMILY.
 DR PIR; S05031; S05031.
 DR Interpro; IPR01417; -.
 DR PROSITE; PS00337; CYTOCHROME B559; PARTIAL.
 KW Photosystem II; Heme; Electron transport; Transmembrane.
 FT DOMAIN 1 18 STROMAL (POTENTIAL).
 FT TRANSMEM 1.9 >21 POTENTIAL.
 FT NON_TER 21 21 SQ SEQUENCE 21 AA; 2331 MW; F22B51A673023CC9 CRC64;

Query Match 26.1%; Score 23; DB 1; Length 21;
 Best Local Similarity 50.0%; Pred. No. 5.4e+02;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 VSGNLTIRUTA 13
 ||| | :|||
 Db 10 VSTPPIFTVXXVA 21

RESULT 5
 PRPL_RAT ID PRPL_RAT STANDARD; PRT; 23 AA.
 AC P10165;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE ACTIC PROLINE-RICH PROTEIN PRP18 PRECURSOR (FRAGMENT).
 OS Ratmus norvegicus (Rat);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parotid gland; PubMed=3840480;
 RX Clements S., Mehansho H., Carlson D.M.;
 RT "Novel multigene families encoding highly repetitive peptide
 sequences. Sequence analyses of rat and mouse proline-rich protein
 CDNA's.";
 RT
 RL J. Biol. Chem. 260:13471-13477(1985).

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 CC or send an email to license@isb-sib.ch).

DR M11899; AAA1956.1;
 KW Repeat; Parotid gland; Multigene family; Saliva; Signal.

FT SIGNAL	1	?	>23	?	ACIDIC PROLINE-RICH PROTEIN PRP18.		RA Flengsrød R., Skjeldal L.;
FT CHAIN	?	23	23	23			RT "Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
FT NON_TER	23						RT Electrophoresis 19:802-806 (1998).
FT SEQUENCE	23 AA;	2380 MW;	875B4F61FD056949 CRC64;				RL -1 - CATALYTIC ACTIVITY: ATP + 3'-PHOSPHO-D-GLYCERATE = ADP + CC 3'-PHOSPHO-D-GLYCEROYL PHOSPHATE.
Query Match	26.18;	Score 23;	DB 1;	Length 23;			CC -1 - PATHWAY: SECOND STEP IN THE SECOND PHASE OF GLYCOLYSIS.
Best Local Similarity	55.68%	Pred. No. 6e+02;					CC -1 - SUBUNIT: MONOMER (BY SIMILARITY).
Matches 5;	Conservative	2;	Mismatches 2;	Indels 0;	Gaps 0;		CC -1 - SUBCELLULAR LOCATION: CYTOPLASMIC.
Qy 6 ITLIRLTA 14	: :						CC -1 - MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 5.6, ITS MW IS: 56.2 KDA.
Db 1 MLVVLTTAA 9							CC -1 - SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
RESULT 6							DR InterPro; IPR001576;
TPX_CLOPA							DR PROSITE; PS00111; PGLYCERATE_KINASE; PARTIAL.
ID TPX_CLOPA							KW Transferase; Kinase; Glycolysis.
AC P81361;							FT NONTER 20 AA; 20
DT 15-JUL-1998	(Rel. 36, Created)						FT 20 AA; 20
DT 15-JUL-1998	(Rel. 36, Last sequence update)						SQ 2355 MW; 749E31E595C85529 CRC64;
DE PROTHIOL PEROXIDASE (EC 1.11.1.-) (CP 42) (FRAGMENT).							
OS Clostridium pasteurianum.							
BC Bacterium; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;							
OC Clostridium.							
OX NCBI_TaxID=1501;							
RN [1]							
RP SEQUENCE.							
RC STRAIN=W5;							
RD MEDLINE=98291870; PubMed=9628918;							
RA Flengsrød R., Skjeldal L.;							
RT "Two dimensional gel electrophoresis separation and N-terminal Electrophoresis 19:802-806 (1998).							
RL 15-JUL-1998 (Rel. 36, Last annotation update)							
DE PROTHIOL PEROXIDASE (EC 1.11.1.-) (CP 42) (FRAGMENT).							
OS Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;							
BC Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Amphiibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;							
OX NCBI_TaxID=39405;							
RN [1]							
RP SEQUENCE, AND MASS SPECTROMETRY.							
RC TISSUE=Parotoid gland;							
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;							
RT "Peptides from Australian frogs. The structures of the caerins and caeridins from <i>Litoria gilleni</i> ." The structures of the caerins and caeridins from <i>Litoria gilleni</i> . J. Chem. Res. 139:937-961 (1993).							
RL 15-JUL-1998 (Rel. 36, Last sequence update)							
DE CAERIDIN 2.							
OS Litoria gilleni.							
BC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;							
OX NCBI_TaxID=39405;							
Query Match 25.0%; Score 22;	DB 1;	Length 20;					Query Match 22.7%; Score 20;
Best Local Similarity 40.0%; Pred. No. 7.7e+02;							Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4;	Conservative	3;	Mismatches 3;	Indels 0;	Gaps 0;		Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TVGNILTR 10	: :						DR 2 VSGNLL 7
Db 4 TFGQNEVTLQ 13							DR 1
RESULT 7							DR 5 VVGNLL 10
TPX_CLOPA							
ID PGK_CLOPA							
AC P81346;							
DT 15-JUL-1998 (Rel. 36, Created)							
DT 15-JUL-1998 (Rel. 36, Last sequence update)							
DT 15-JUL-1998 (Rel. 36, Last annotation update)							
DE PUTATIVE PHOSPHOGLYCERATE KINASE (EC 2.7.2.3) (CP 11) (FRAGMENT).							
GN PGK.							
OS Clostridium pasteurianum.							
BC Bacterium; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;							
OC Clostridium.							
OX NCBI_TaxID=1501;							
RN [1]							
RP SEQUENCE.							
RC STRAIN=W5;							
RX MEDLINE=98291870; PubMed=9629918;							

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE LEU_A LEADER PEPTIDE.

GN LEU_A.

OS Corynebacterium glutamicum (Brevibacterium flavidum).

OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Corynebacteriaceae;

OC Corynebacterium.

OX NCBI_TAXID=1718;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=PATCC 13032; PubMed=8117072;

RX MEDLINE=94161495; PubMed=8117072;

RA Pacak M., Krumbach K., Eggeling L., Sahm H.;

RT "Leucine synthetase in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis.";

RT AppL. Environ. Microbiol. 60:133-140(1994).

CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS OF LEUCINE (BY SIMILARITY).

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CC EMBL: X70959; CAA0295.1; ALT_TERM.

KW Leader peptide; Leucine biosynthesis

SEQUENCE 22 AA; BB6E3DA6604AD7F8 CRC64;

Query Match 22.7%; Score 20; DB 1; Length 22;

Best Local Similarity 40.0%; Pred. No. 1.3e+03; Matches 4; Conservative 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 6 T\$TRANLLR 15

RESULT 10

PAP1_MANSE STANDARD; PRT; 23 AA.

AC P30253;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE PARALYTIC PEPTIDE I (PP I).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

OC Pieridae; Neoptera; Endopterygota; Lepidoptera; Hexapoda; Insecta;

OC Sphingidae; Sphingidae; Sphinginae; Manduca.

NCBI_TAXID=7130;

[1]

RP SEQUENCE.

RT TISSUE=hemolymph; PubMed=2071576;

RX MEDLINE=911302298; Skinner W.S., Dennis P.A., Li J.P., Summerfelt R.M., Carney R.L., Quistad G.B.; "Isolation and identification of paralytic peptides from hemolymph of the lepidopteran insects *Manduca sexta*, *Spodoptera exigua*, and *Heliothis virescens*"; J. Biol. Chem. 266:12873-12877(1991).

CC -!- FUNCTION: CAUSES RAPID, RIGID PARALYSIS WHEN INJECTED INTO LEPIDOPTERAN LARVAE. THE PHYSIOLOGICAL ROLE MAY BE TO REDUCE HEMOLYMPH LOSS FOLLOWING INJURY AND PROMOTE WOUND HEALING.

CC -!- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.

DR A39855; A39855.

KW Hemolymph.

FT DISULFID 7 19 BY SIMILARITY.

SEQUENCE 23 AA; 2436 MW; 0B26CB5C29855PE4 CRC64;

Query Match 22.7%; Score 20; DB 1; Length 23;

Best Local Similarity 40.0%; Pred. No. 2e+03; Matches 8; Indels 0; Gaps 0;

Qy 3 SGNLTIRPAADHR 17
Db 4 AGGCATGYLTADGR 18

RESULT 11

BGBP_PENVA STANDARD; PRT; 25 AA.

ID BGBP_PENVA
AC P81182;

RT 15-JUL-1998 (Rel. 36, Last sequence update)

RT 15-JUL-1998 (Rel. 36, Last annotation update)

RT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Beta-1,3-D-GLUCAN BINDING PROTEIN (BGBP) (FRAGMENT).

OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Penaeidae; Penaeus.

NCBI_TAXID=6689;

RP SEQUENCE.

RX MEDLINE=9729346; PubMed=9149398;

RA Vargas-Albores F., Jimenez-Vega F., Yepiz-Plascencia G.M.;

RT "Purification and comparison of beta-1,3-glycan binding protein from white shrimp (*Penaeus vannamei*)."; Comp. Biochem. Physiol. 116B:453-458(1997).

CC -!- FUNCTION: INVOLVED IN THE RECOGNITION OF INVADING MICRO-ORGANISMS.

CC -!- SUBUNIT: MONOMER.

FT NON-TER 25 25 AA; 2743 MW; 747DD77EDC0FB06F CRC64;

SEQUENCE 25 AA; 2743 MW;

Query Match 22.7%; Score 20; DB 1; Length 25;

Best Local Similarity 30.0%; Pred. No. 2.2e+03; Matches 3; Conservative 5; Indels 2; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 6 SLAGNFNSLR 15

RESULT 12

Y15_BPT3 STANDARD; PRT; 25 AA.

ID Y15_BPT3
AC P20835;

RT 01-FEB-1991 (Rel. 17, Created)

RT 01-FEB-1991 (Rel. 17, Last sequence update)

RT 01-FEB-1991 (Rel. 17, Last annotation update)

DE HYPOTHETICAL GENE 1.5 PROTEIN.

GN 1.5.

OS Bacteriophage T3.

OC dsDNA viruses, no RNA stage; Tailed phages; Podoviridae;

OC T7-like phages;

OX NCBI_TAXID=10739;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LURIA;

RX MEDLINE=87226207; PubMed=3586029;

RA Schmitt M.P., Beck P.J., Kearney C.A., Spence J.L., Di Giovanni D., Condray J.P., Molineux I.J.;

RT "Sequence of a conditionally essential region of bacteriophage T3, including the primary origin of DNA replication.";

RT RL J. Mol. Biol. 193:479-495(1987).

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CC EMBL; X17255; CAA35126.1; -;
 DR EMBL; X05031; CAA28701.1; -;
 DR PIR; S09540;
 KW HYPOTHETICAL protein;
 SQ SEQUENCE 25 AA; 2821 MW; 92B7709153A2950A CRC64;

Query Match 22.7%; Score 20; DB 1; Length 25;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 ILTIRATAAD 15
 Db 9 VATGLGMVAD 18

RESULT 13
 TEMD_RANTE STANDARD PRT; 13 AA.

ID TEMD_RANTE STANDARD; PRT; 13 AA.
 AC P56918;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TEMPORIN_C.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.

NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barri D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).

-!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 CC BACTERIA.
 -!- SUBCELLULAR LOCATION: SECRETED.

-!- SIMILARITY: BELONGS TO THE BREVININ/ESCOLVENTIN/GAEGRIN/RUGOSIN
 FAMILY.
 KW Amphibian skin; Antibiotic; Amidation; Multigene family.

FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1363 MW; 2201403A655B2448 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSGNIL 7
 Db 4 IIGNIL 9

RESULT 14
 TEMD_RANTE STANDARD PRT; 13 AA.
 ID TEMD_RANTE STANDARD; PRT; 13 AA.
 AC P56919;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TEMPORIN_D.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.

NCBI_TaxID=8407;
 RN [1]

RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Skin;
 RX MEDLINE=97175050; PubMed=9022710;

RA Barri D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 -!- FUNCTION: HAS NO ANTIBACTERIAL ACTIVITY.

CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCOLVENTIN/GAEGRIN/RUGOSIN
 FAMILY.

KW Amphibian skin; Amidation; Multigene family.

FT MOD_RES 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1379 MW; 3EF55DFA655B2448 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSGNIL 7
 Db 4 IIGNIL 9

RESULT 15
 TEME_RANTE STANDARD PRT; 13 AA.
 ID TEME_RANTE STANDARD; PRT; 13 AA.
 AC P56920;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TEMPORIN_E.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
 NCBI_TaxID=8407;
 RN [1]

RP SEQUENCE.

RC TISSUE=Skin;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barri D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).
 -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 CC BACTERIA.

-!- SIMILARITY: BELONGS TO THE BREVININ/ESCOLVENTIN/GAEGRIN/RUGOSIN
 FAMILY.
 KW Amphibian skin; Antibiotic; Amidation; Multigene family.

FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1379 MW; 265505DFA79A92448 CRC64;

Query Match 21.6%; Score 19; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSGNIL 7
 Db 4 IIGNIL 9

RESULT 14
 TEMD_RANTE STANDARD PRT; 13 AA.
 ID TEMD_RANTE STANDARD; PRT; 13 AA.
 AC P56919;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE TEMPORIN_D.
 OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.

NCBI_TaxID=8407;
 RN [1]

Search completed: May 8, 2001, 15:14:10
 Job time: 531 sec

GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: May 8, 2001, 15:16:08 ; Search time 114.89 Seconds
(without alignments)
18.363 Million cell updates/sec

Title: US-09-165-546A-13
Perfect score: 88
Sequence: 1 TVSGNLTIRUTAHDHQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 37470 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 6627

Minimum DB seq length: 0
Maximum DB seq length: 25 .

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_invertebrate:*
- 5: sp_human:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	38 6	19 14	Q69345	069345 human herpe
2	33	37.5	20 2	Q9R4Y1	Q9R4Y1 proeius vul
3	28	31.8	20 11	Q9QV28	Q9QV28 rattus sp.
4	27	30.7	18 2	Q53503	Q53503 lactobacill
5	27	30.7	24 2	Q54460	Q54460 erwinia her
6	27	30.7	25 11	Q9QV49	Q9QV49 rattus sp.
7	26	29.5	15 2	Q53541	Q53541 bacillus sp
8	26	29.5	23 6	Q28016	Q28016 bos taurus
9	25	28.4	15 1	Q9UWH9	Q9UWH9 thermococcus
10	25	28.4	19 1	Q9UWL8	Q9UWL8 thermoplasma
11	25	28.4	25 14	Q9PXH2	Q9PXH2 human t-cell
12	24	27.3	15 11	Q9R5694	Q9R5694 mus musculus
13	24	27.3	19 11	Q9QV90	Q9QV90 mus sp. mep
14	24	27.3	20 2	Q9RN1	Q9RN1 rhodococcus
15	24	27.3	20 6	Q9TRM1	Q9TRM1 bos taurus
16	24	27.3	20 11	Q9QW31	Q9QW31 rattus sp.
17	24	27.3	23 6	Q29394	Q29394 canis famili
18	24	27.3	25 14	Q9PXH3	Q9PXH3 human t-cell
19	23	26.1	13 2	Q9R5U4	Q9R5U4 pseudomonas

ALIGNMENTS

RESULT	2	23	26.1	16	2	Q52901	rhizobium m	
		22	23	26.1	17	7	Q31213	oncorhynchus
		23	23	26.1	18	3	Q01672	pneumocystis
		24	23	26.1	18	3	Q02414	aspergillus
		25	23	26.1	19	14	Q84197	human respi
		26	23	26.1	20	10	Q9S900	virginiana sinen
		27	23	26.1	21	4	Q9UC66	homo sapien
		28	23	26.1	21	14	Q9yq58	porcine cir
		29	23	26.1	21	14	Q56126	porcine cir
		30	22	25.0	12	10	Q9S931	sambucus ni
		31	22	25.0	16	6	P79137	cercopithecus
		32	22	25.0	18	14	Q9OkJ7	human immun
		33	22	25.0	22	11	Q9OnS7	Q9qk77
		34	22</					

DR INTERPRO; IPR000626; -
 DR PFAM; PF00240; ubiquitin; 1.
 SQ SEQUENCE 25 AA; 2808 MW; E22C0441310AA50D CRC64;

Query Match 30.7%; Score 27; DB 11; Length 25;
 Best Local Similarity 26.7%; Pred. No. 6e+02;
 Matches 4; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 Non_TER 15; Sequence 15 AA; 1529 MW; 5BADC7F1318F3B3C CRC64;

RESULT 7
 ID Q53541; PRELIMINARY; PRT; 15 AA.
 AC Q53541; 1:1 :1: ;|: ;|:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE ORF2 PROTEIN (FRAGMENT).
 OS Bacillus sp.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 NCBI_TaxID=1409; NCBI_TaxID=1409;
 RN 1
 RP SEQUENCE FROM N.A.; MEDLINE=93400017; PubMed=7670201;
 RA Seto Y., Hashimoto M., Usami R., Hamamoto T., Kudo T., Horikoshi K.;
 RT "Characterization of a mutation responsible for an alkali-sensitive mutant, 18224, of alkaliphilic Bacillus sp. strain C-125.";
 RL Biosci. Biotechnol. Biochem. 59:1364-1366(1995).
 DR EMBL; S79441; AAB3556.1; --.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1529 MW; 5BADC7F1318F3B3C CRC64;

Query Match 29.5%; Score 26; DB 2; Length 15;
 Best Local Similarity 58.3%; Pred. No. 5.2e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Non_TER 15; Sequence 15 AA; 1529 MW; 5BADC7F1318F3B3C CRC64;

RESULT 10
 ID Q90WL8; PRELIMINARY; PRT; 19 AA.
 AC Q90WL8; 1:1 :1: ;|: ;|:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE UBQUITIN (FRAGMENT).
 OS Thermoplasma acidophilum,
 Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmae;
 OC Thermoplasma.
 NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE.

Query Match 28.4%; Score 25; DB 1; Length 19;
 Best Local Similarity 30.8%; Pred. No. 1e+03;
 Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Non_TER 1 1
 SQ SEQUENCE FROM N.A.; MEDLINE=9432479; PubMed=8835545;
 RA Moody D.E., Pomp D., Barendse W.;
 RT "Linkage mapping of the bovine insulin-like growth factor-1 receptor gene.";
 RL Mamn. Genome 7:168-169(1996).
 DR EMBL; U33122; AAB52601.1; --.
 FT NON_TER 1 1
 SQ SEQUENCE 23 AA; 2458 MW; D9814EC8DB0FE853 CRC64;

RESULT 11 Q9PXH2 ID Q9PXH2 AC Q9PXH2; DT 01-MAY-2000 (TREMBLrel. 13, Created) DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update) DE VARIANT TRANSACTIVATION FACTOR (FRAGMENT). OS Human T-cell lymphotropic virus type 1. OC viruses; Retroviridae; BLV-HTLV retroviruses. RN NCBI_TaxID=11908; RP SEQUENCE FROM N.A.; PubMed=7533860; RX MEDLINE=95191051; PubMed=7533860; SQ 25 AA; 2638 MW; CF0FFBD4DDBB51D26 CRC64;	Query Match Score 24; DB 11; Length 15; Best Local Similarity 66.7%; Pred. No. 1.2e+03; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; PRT; 25 AA.	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update) DE MEPIN-A PEPTIDE A2. OS Mus sp. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10095; RN [1] RP SEQUENCE. RX MEDLINE=91173354; PubMed=1894622; RA Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S., "Meprin-A and -B: Cell surface endopeptidases of the mouse kidney."; RT J. Biol. Chem. 266:17350-17357(1991). RL SEQUENCE 19 AA; 1943 MW; DD08DIAB5B71051 CRC64;
RESULT 12 Q05694 ID Q05694 AC Q05694; DT 01-NOV-1996 (TREMBLrel. 01, Created) DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update) DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update) DE PROLINE-RICH PROTEIN MP6 (FRAGMENT). GN MP6. OS MUS MUSCULUS (Mouse). OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; RN [1] RP SEQUENCE FROM N.A.; RC STRAIN=DALB/C; MEDLINE=92020406; PubMed=1747160; RA Roberts S.G.E., Layfield R., McDonald C.J.; RT "The mouse proline-rich protein MP6 promoter binds isoprenaline-inducible parotid nuclear proteins via a highly conserved NFkB/rel-like site."; RT Nucleic Acids Res 19:5205-5211(1991). DR EMBL; X61126; CAA3438_1; -. FT NON-TER 15 SQ SEQUENCE 15 AA; 1557 MW; C0FF9514A8F70EE4 CRC64;	Query Match Score 25; DB 14; Length 25; Best Local Similarity 43.8%; Pred. No. 1.3e+03; Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1; PRT; 25 AA.	Query Match Score 24; DB 11; Length 19; Best Local Similarity 42.9%; Pred. No. 1.5e+03; Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0; PRT; 20 AA.
RESULT 13 Q9QVK0 ID Q9QVK0 AC Q9QVK0; DT 01-MAY-2000 (TREMBLrel. 13, Created)	Query Match Score 24; DB 11; Length 15; Best Local Similarity 66.7%; Pred. No. 1.2e+03; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; PRT; 25 AA.	Query Match Score 27.3%; DB 11; Length 15; Best Local Similarity 66.7%; Pred. No. 1.2e+03; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; PRT; 20 AA.
Q9QVK0 ID Q9QVK0 AC Q9QVK0; DT 01-MAY-2000 (TREMBLrel. 13, Created)	Query Match Score 24; DB 11; Length 15; Best Local Similarity 66.7%; Pred. No. 1.2e+03; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; PRT; 25 AA.	Query Match Score 27.3%; DB 11; Length 15; Best Local Similarity 66.7%; Pred. No. 1.2e+03; Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0; PRT; 20 AA.

Tue May 8 15:56:35 2001

us-09-165-546a-13.rspt

Page 5

RX MEDLINEP=93015942; PubMed=1400371;
RA Kojima K., Ogawa H.K., Seno N., Yamamoto K., Irimura T., Osawa T.,
RA Matsunoto I.;
PT "Carbohydrate-binding proteins in bovine kidney have consensus amino
acid sequences of annexin family proteins.";
RL J. Biol. Chem. 267:20536-20539(1992).
DR HSSP; P13214; IANIN.
SQ SEQUENCE 20 AA: 2107 MW: 45BA0EBB451A5C92 CRC64:

Query Match 27.3%; Score 24; DB 6; Length 20;
Best Local Similarity 55.6%; Pred. No. 1.6e+03; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 3;
OY 5 NILTIRUTA 13
| : | |
Db 11 NWLAYRSTA 19

Search completed: May 8, 2001, 15:16:09
Job time: 535 sec